

## 10B15 SEARCH REQUEST FORM 75-475

Requestor's Name: John Wm Serial Number: 08/918874  
 Date: 5-14-98 Phone: 308-4008 Art Unit: 1646

## Search Topic:

Please write a detailed statement of search topic. Describe specifically as possible the subject matter to be searched. Define any terms that may have a special meaning. Give examples or relevant citations, authors keywords, etc., if known. For sequences, please attach a copy of the sequence. You may include a copy of the broadest and/or most relevant claim(s).

Please search SEQ ID NO: 1 + 2

of 08/918874.

## STAFF USE ONLY

Date completed: 5/18  
 Searcher: 82308-4292 Search Site: STIC Vendors: IG Suite  
 Terminal time: 5 ✓ CM-1 STN  
 Elapsed time: props Pre-S Dialog  
 CPU time: 1 Type of Search APS  
 Total time: 1 N.A. Sequence Geninfo  
 Number of Searches: 1 A.A. Sequence SDC  
 Number of Databases: 7 Structure DARC/Questel  
Bibliographic ✓ Other MBrch

\*\*\*\*\*  
 M A S R C H (TM)  
 \*\*\*\*\*

Release 3.0.SAA John F. Collins, Biocomputing Research Unit.  
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MPerch\_n n.a. - n.a. database search, using Smith-Waterman algorithm

Run on: Fri May 15 17:45:22 1998; MasPar time 2128.68 Seconds  
 1495.787 Million cell updates/sec

Tabular output not generated.

Title: >US-08-918-874-2  
 Description: (1-2082) from US08918874.seq  
 Perfect Score: 2082  
 N.A. Sequence: 1 CCAACTGCACCTGGTCTCA.....CATTTTATATGCTTACTA 2082  
 Comp: GGTTCACGTGGAGCCAGAT.....GTAAATATACGAAATGAT

Scoring table: TABLE default  
 Gap 6

Nmatch STD : Dbase 0; Query 0

Searched: 436399 seqs, 746661465 bases x 2

Post-processing: Minimum Match 0%  
 Listing first 45 summaries

Database: embl53  
 1:em\_in 2:em\_or 3:em\_on 4:em\_ov 5:em\_pl 6:em\_htg  
 7:em\_hum1 8:em\_hum2 9:em\_ba 10:em\_ro 11:em\_un 12:em\_vi  
 13:em\_pt  
 Database: genbank105  
 14:gb\_ro 15:gb\_on 16:gb\_ov 17:gb\_in 18:gb\_pl 19:gb\_ba  
 20:gb\_st 21:gb\_vi 22:gb\_ph 23:gb\_sy 24:gb\_un 25:gb\_pt  
 26:gb\_htg 27:gb\_pr1 28:gb\_pr2

Statistics: Mean 11.767; Variance 5.428; scale 2.168

Pred. No. is the number of results predicted by chance to have a  
 score greater than or equal to the score of the result being printed,  
 and is derived by analysis of the total score distribution.

#### SUMMARIES

Result	No.	Score	Match	Length	DB	ID	Description	Pred. No.
1	1776	85.3	1804	28	AF029761		Homo sapiens decoy rec	0.00e+00
2	1161	55.8	1161	28	AF023849		Homo sapiens TNF recep	0.00e+00
3	390	18.7	1180	28	AF012536		Homo sapiens decoy rec	0.00e+00
4	390	18.7	1377	28	AF033854		Homo sapiens lymphocyt	0.00e+00
5	388	18.6	900	28	AF020502		Homo sapiens cytotoxic	0.00e+00
6	386	18.5	1388	28	AF016267		Homo sapiens TRAIL rec	0.00e+00
7	345	16.6	780	28	AF012629		Homo sapiens autophan	1.22e-273
8	264	12.7	1323	28	AF018658		Homo sapiens apoptosis	3.16e-200
9	265	12.7	3993	28	AF016266		Homo sapiens TRAIL rec	3.97e-201
10	259	12.4	1859	28	AF016849		Homo sapiens autophan	1.01e-195
11	202	9.7	1407	28	HS090875		Human cytotoxic ligand	1.06e-144
12	195	9.4	1236	28	AF020501		Homo sapiens cytotoxic	1.75e-138
13	195	9.4	1236	28	AF018657		Homo sapiens cytotoxic	1.75e-138
14	196	9.4	1717	28	AF016268		Homo sapiens death rec	2.27e-139

15	194	9.3	1799	28	AF012535		Homo sapiens death rec	1.35e-137
16	191	9.2	1236	28	AF012628		Homo sapiens death dom	6.14e-135
17	191	9.2	1236	28	AF023866		Homo sapiens p53-regul	6.14e-135
18	96	4.6	92975	28	AC002369		Homo sapiens Xp22 PAC	8.54e-53
19	93	4.5	99207	28	HS102620		Human DNA sequence fro	2.63e-50
20	93	4.5	148451	26	AC004031		Homo sapiens; HTGS pha	2.63e-50
21	93	4.5	149490	28	HS095740		Human chromosome 16p13	2.63e-50
22	94	4.5	173767	28	AC002449		Human PAC clone D404K	3.90e-51
c 23	92	4.4	63369	26	AC002413		*** SEQUENCING IN PROG	1.77e-49
24	92	4.4	61960	28	HS9649		Human DNA sequence fro	1.77e-49
c 25	91	4.4	153460	28	HS052111		Homo sapiens Xq28 geno	1.18e-48
26	92	4.4	165279	26	HS262D12		Human DNA sequence ***	1.77e-49
c 27	89	4.3	15913	28	HSALADG		H. sapiens ALAD gene fo	5.25e-47
28	90	4.3	34352	28	U73638		Human chromosome 11 Co	7.89e-48
c 29	89	4.3	40491	28	AC002116		Human DNA from chromos	5.25e-47
30	89	4.3	93273	28	AC004084		Homo sapiens BAC clone	5.25e-47
c 31	90	4.3	139034	26	HS050815		Human DNA sequence ***	7.89e-48
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c 40	88	4.2	43726	26	HSN102C10		Human DNA sequence ***	3.49e-46
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c 43	88	4.2	172994	28	HS051318		Human chromosome 16p13	3.49e-46
44	88	4.2	179544	28	AF015720		Homo sapiens chromosom	3.49e-46
45	88	4.2	219447	27	HUMFLNGP6D		Homo sapiens chromosom	3.49e-46

#### ALIGNMENTS

RESULT	1	LOCUS	AF029761	1804 bp	mRNA	PRI	16-DEC-1997
DEFINITION	Homo sapiens decoy receptor 2 mRNA, complete cds.						
ACCESSION	AF029761						
NID	g2688980						
KEYWORDS							
SOURCE	human.						
ORGANISM	Homo sapiens						
REFERENCE	Eukaryotae; Metazoa; Chordata; Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.						
AUTHORS	1 (bases 1 to 1804)						
TITLE	A Novel Receptor for Apo2L/TRAIL Contains a Truncated Death Domain						
JOURNAL	Curr. Biol. (1997) In press						
REFERENCE	2 (bases 1 to 1804)						
AUTHORS	Marsters,S.A., Sheridan,J.P., Pitti,R.M., Huang,A., Skubatch,M., Baldwin,D., Yuan,J., Gurney,A., Goddard,A.D., Godowski,P. and Ashkenazi,A.						
TITLE	Direct Submission						
JOURNAL	Submitted (14-OCT-1997) Molecular Oncology, Genentech, 1 DNA Way, South San Francisco, CA 94080, USA						
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BASE COUNT 454 a 462 c 460 g 428 t  
ORIGIN

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Best Local Similarity 99.74; Pred. No. 0.00e+00;  
Matches 1799; Conservative 1; Mismatches 0; Indels 4; Gaps 1;

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Qy 1 CCAACTGCACTCGGTTCATGCTGAATTCCTCCCGGGATCTCTAGAGATCCCTCGAC 60

Db 61 CTGACCCACGCGCTCGCGGAGAACTTTGACGCGCAACAACCTACGGGAGCATTTCTG 120

Qy 61 CTGACCCACGCGCTCGCGGAGAACTTTGACGCGCGCAACAACCTACGGGAGCATTTCTG 116

Db 121 ATGATTTTGGGCGCTTCGATCCACCTCTCTCCCTCTCATAGGATTTTGGGGCAAG 180

Qy 117 ATGATTTTGGGCGCTTCGATCCACCTCTCTCCCTCTCATAGGATTTTGGGGCAAG 176

Db 181 GGTTCGACCGCTCGAGCGCTCGAGAGGGCGCTATCAGAGAGCGAGACAGGTGCGG 240

Qy 177 GGTTCGACCGCTCGAGCGCTCGAGAGGGCGCTATCAGAGAGCGAGACAGGTGCGG 236

Db 241 AACCAAGCACTGGCTCTGAGACCCAGATCTTAAGTGTGCGTCTCATGTGCGGCT 300

Qy 237 AACCAAGCACTGGCTCTGAGACCCAGATCTTAAGTGTGCGTCTCATGTGCGGCT 296

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Db 361 GACAGTGGCCCAACACACAGAGCGACGCTCAAGGAGGAGGATGTCACGACGATC 420

Qy 357 GACAGTGGCCCAACACACAGAGCGACGCTCAAGGAGGAGGATGTCACGACGATC 416

Db 421 TCTATAGTACAGTAATACTGAGGCTGTAAACCGTGCACAGAGGTGTGATATACACCT 480

Qy 417 TCTATAGTACAGTAATACTGAGGCTGTAAACCGTGCACAGAGGTGTGATATACACCT 476

Db 481 TGTCTTCAACAATTTGCTTCTTGGCTGCTATGTACAGTTTAAATCAGGTCAACAAA 540

Qy 477 TGTCTTCAACAATTTGCTTCTTGGCTGCTATGTACAGTTTAAATCAGGTCAACAAA 536

Db 541 TAAAGTTCCTGTACACACGACAGACACCGTGTGAGTGTGAAAGGAGGTTCOA 600

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Qy 597 GGAATAAAATCCCTCGAGATGTGCGGACGCTGTAGAAGAGGTGTCACGAGGATG 656

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Qy 717 TTCACTGGGAAACCCACAGCGAGGAGACAGTACCACCTCTGGGGATGCTTCG 776

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Qy 777 CTCTCCCTATCACTACTTATCATCATAGTGGTTTGTAGTCATCAATTTAGCTGGTGT 836

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Qy 897 TGGAGAGGTCCCGAACGTTGTGCACAGAGCTCTTTTCCGCGCGGCTCATGTCTCTCAG 956

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Qy 1017 CACCCAGGTCTCTGACGAGGAATCAAGGTGACGAGCTGACAGAGCTAACAGGTGTGAC 1076

Db 1081 TGTAGAGTGCACAGAGAGCCACAGCTCTGTCGAAACAGCGAAGCTGAAGGCTGCA 1140

Qy 1077 TGTAGAGTGCACAGAGAGCCACAGCTCTGTCGAAACAGCGAAGCTGAAGGCTGCA 1136

Db 1141 GAGGAGGAGCTGCTGCTTCCAGTGAATGACGCTGACTGCTGACATCAGACCTTGCT 1200

Qy 1137 GAGGAGGAGCTGCTGCTTCCAGTGAATGACGCTGACTGCTGACATCAGACCTTGCT 1196

Db 1201 GGATGCTTGGCAACACTGGAGAGGACATCAAGGAACAACTTACGAGCACTGGT 1260

Qy 1197 GGATGCTTGGCAACACTGGAGAGGACATCAAGGAACAACTTACGAGCACTGGT 1256

Db 1261 GGGCTCGGAAAGACTCTTTATGAGAGAGTGGAGGAGCTGCTGCTGCTGCTGCTG 1320

Qy 1257 GGGCTCGGAAAGACTCTTTATGAGAGAGTGGAGGAGCTGCTGCTGCTGCTGCTG 1316

Db 1321 AAGAGATCTCTCAGGAACACAGAGCTGCTCCTATTATCTCTCTCCTCAAGGGAAG 1380

Qy 1317 AAGAGATCTCTCAGGAACACAGAGCTGCTCCTATTATCTCTCTCCTCAAGGGAAG 1376

Db 1381 CAGCTCGGAAAGAACTGCCAGTCTGAGCCATGCCCAAGAACTCTACTATCATA 1440

Qy 1377 CAGCTCGGAAAGAACTGCCAGTCTGAGCCATGCCCAAGAACTCTACTATCATA 1436

Db 1441 TGGGCGAGTTACCAATGGTCTAGAACTTGTGTAACGCACTTGGAGTAATTTATGAA 1500

Qy 1437 TGGGCGAGTTACCAATGGTCTAGAACTTGTGTAACGCACTTGGAGTAATTTATGAA 1496

Db 1501 ATACTGCTGTGTAAGCAAAACGGGAAATTTATACAGATCTTGCTGCTATGAT 1560

Qy 1497 ATACTGCTGTGTAAGCAAAACGGGAAATTTATACAGATCTTGCTGCTATGAT 1556

Db 1561 ACAGTGTGTATTAAGGCTGTTTATAGCCACATGCGGTGCTCATGCTGTATCCAG 1620

Qy 1557 ACAGTGTGTATTAAGGCTGTTTATAGCCACATGCGGTGCTCATGCTGTATCCAG 1616

Db 1621 CACTTTGATAGGCTGAGGCGAGGTGATGCTTGCTGAGCTGGGAGTTTGAGACCGCTCAT 1680

Qy 1617 CACTTTGATAGGCTGAGGCGAGGTGATGCTTGCTGAGCTGGGAGTTTGAGACCGCTCAT 1676

Db 1681 CAACACAGTGAATCCATCTCAATTTTAAAAAGAAAGAGGTGTTTAGGTGTCAATC 1740

Qy 1677 CAACACAGTGAATCCATCTCAATTTTAAAAAGAAAGAGGTGTTTAGGTGTCAATC 1736

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Qy 1737 TTTCAGTCTTCTCATCATGAGACAGTCTTTTTTCTGCTCTTATATTGCAAGTCCAT 1796

Db 1801 CTCT 1804

Qy 1797 CTCT 1800

RESULT 2  
LOCUS AF023849 1161 bp mRNA PRI 01-DEC-1997

DEFINITION Homo sapiens TNF receptor-related receptor for TRAIL mRNA, complete cds.

ACCESSION AF023849

NID g2653844

KEYWORDS

SOURCE human.  
 ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Vertebrata; Mammalia; Eutheria;  
 Primates; Catarrhini; Hominidae; Homo.  
 REFERENCE 1 (bases 1 to 1161)  
 AUTHORS Pan, G.  
 TITLE TRUND, a new member of the TRAIL receptor family that antagonizes  
 TRAIL signalling  
 JOURNAL Unpublished  
 REFERENCE 2 (bases 1 to 1161)  
 AUTHORS Pan, G., M. J. and Dixit, V. M.  
 TITLE Direct Submission  
 JOURNAL Submitted (10-SEP-1997) Pathology, University of Michigan, 1301  
 Catherine Road, MSB1, RM7520, Ann Arbor, MI 48109, USA  
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 Matches 1160; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

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 Qy 217 GGAGCAGGACAGCGTGGGAAACAGACATGGCTCTGCGACCCCAAGATGCTTAAAGTC 276  
 Db 121 GTGCTCTCATGCTCGCGGGTCTGCTGCGGGTCCGGGTGACTCTGCACCATCCCCGG 180  
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 Db 901 CGACAGCTAACAGGTGTGACTGTAGACTGCCAGAGAGCAGACAGCTCTGCTGGAACG 960  
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RESULT 3  
 LOCUS AF012536 1180 bp mRNA PRI 21-AUG-1997  
 DEFINITION Homo sapiens decoy receptor 1 (DcR1) mRNA, complete cds.  
 ACCESSION AF012536  
 NID g2338421  
 KEYWORDS  
 SOURCE human.  
 ORGANISM Homo sapiens  
 Eukaryota; mitochondrial eukaryotes; Metazoa; Chordata;  
 Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominidae;  
 Homo.  
 REFERENCE 1 (bases 1 to 1180)  
 AUTHORS Sheridan, J. P., Marsters, S. A., Pitti, R. M., Gurney, A., Skubatch, M.,  
 Baldwin, D., Ramakrishnan, L., Gray, C. L., Baker, K., Wood, W. I.,  
 Goddard, A. D., Godowski, P., and Ashkenazi, A.  
 TITLE Control of TRAIL-induced apoptosis by a family of signaling and  
 decoy receptors  
 JOURNAL Science 277 (5327), 818-821 (1997)  
 MEDLINE 97390509  
 REFERENCE 2 (bases 1 to 1180)  
 AUTHORS Sheridan, J. P., Marsters, S. A., Pitti, R. M., Gurney, A., Baldwin, D.,  
 Ramakrishnan, L., Gray, C. L., Baker, K., Wood, W. I., Goddard, A. D.,  
 Godowski, P., and Ashkenazi, A.  
 TITLE Direct Submission  
 JOURNAL Submitted (06-JUL-1997) Molecular Oncology, Genentech, 1 DNA Way,  
 South San Francisco, CA 94080, USA

DEFINITION	<p>                     Homo sapiens lymphocyte inhibitor of TRAIL (LIT) mRNA, complete cds.                      AF0313854                      g2645841                      .                      human.                      Homo sapiens                      Eukaryota; Metazoa; Chordata; Vertebrata; Mammalia; Dutheria; Primates; Catta rhini; Homi nidae; Homo.                      1 (bases 1 to 1377)                      Mongkol sapaya, J., Cowper, A., Xu, X., Morris, G., McMichael, A. J., Bell, J. I. and Screaton, G. R.                      Lymphocyte inhibitor of TRAIL: A new receptor protecting lymphocytes from the death ligand TRAIL                      J. Immunol. (1997) in press                      2 (bases 1 to 1377)                      Mongkol sapaya, J., Cowper, A., Xu, X., Morris, G., McMichael, A. J., Bell, J. I. and Screaton, G. R.                      Direct Submission                      Submitted (10-NOV-1997) Immunology, Institute of Molecular Medicine, John Radcliffe Hospital, Headington, Oxford OX3 9DS, UK                 </p>
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BASE COUNT      335 a   409 c   365 g   268 t

ORIGIN

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Query Match 18.7%; Score 390; DB 28; Length 1377;  
Best Local Similarity 83.5%; Pred. No. 0.00e+00;  
Matches 517; Conservative 0; Mismatches 97; Indels 5; Gaps 4;

D<sub>b</sub>     91 GGAAGCTTGGGACAGAGCGCCCGGCCCT-GATGGCCGAGGCAGGGTGCAACCAGG 149  
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Q<sub>y</sub>    159 GGGACTTTGGGACAAGCGTCGCCGACCGCTCGAGCGCTCAGCAGGGCGCTATCCAGG 218

D<sub>b</sub> 150 ACCCAGGACGGCGTCGGGAACCATAACCATGGC-CCGGATCCCCAAGACCTTAAGTTCGT 208  
| ||||| | ||||||| ||||| || | ||||| || |||||  
Q<sub>y</sub> 219 AGCCAGGACAGCGTCGGGAACCAGACCATGGCTCCTGGACCCAAGATCCTTAAGTTCGT 278

D<sub>b</sub> 209 CGTCGTCATCGTCGCGGTCCTGCTGCCAGTCTTACCTACTCTGCCACCCTGCCCGCGCA 268  
||||| ||||||||| ||||||| |||| | ||||||||| |||||||

Q<sub>y</sub> 279 CGTCTTCATCGTCGCGGTTCTGCTGCCGGTCCGGTTGACTCTGCCACCATCCCCCGCA 338

D<sub>b</sub> 269 GGAGGAAGTTCCTCCACGACAGTAGTGCCCCACAGCAACAGAGGCACAGCTTCAGGGGGA 328  
||| ||||||||||||||||||||||||||||||||||||||| ||| ||||| |||  
Q<sub>y</sub> 339 GGACGAAGTTCCTCCACGACAGTAGTGCCCCACAGCAACAGAGGCCAGCCTCAGGAGGA 398

D<sub>b</sub> 329 GGAGTGTCCAGCAGGATCTCATAGATCAGAACATACTGGAGCCTGTAACCCGTGCACAGA 388  
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Q<sub>y</sub> 399 GGAGTGTCCAGCAGGATCTCATAGATCAGAAATATACTGGAGCCTGTAACCCGTGCACAGA 458

D<sub>b</sub> 389 GGGTGTGGATTACACCAACGCTTCCAACAATGAACCTTCTTGCTTCCCATGTACAGTTTG 448  
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Q<sub>y</sub> 459 GGGTGTGGATTACACCAATTGCTTCCAACAATTTGCCCTTCTTGCTGCTATGTACAGTTTG 518

db 449 TAAATCAGATCAAAAACATAAAAGTTCCTGCACCATGACCAGAGACACAGTGTGTCTAGT 508

[illegible]

Qy 519 TAAATCAAGTCAACAATAAAGTTCCTGTACCAGCAGCAGACCGTGTCAAGT 578  
 Db 509 TAAGAAGGACCACTTCGGAATGAAAACATCCAGAGATGTGCGGAAGTGTAC -CAGG 566  
 Qy 579 TGAAGAAAGAGCTCCAGGATAAAACATCCCTGAGATGTGCGGACGTGTAGAACAGG 638  
 Db 567 -TGCCCTAGTGGGAAGTCCAAGTCAATTAATGTACCTCGGATGATATCAAGTGTGT 625  
 Qy 639 GTGTCCAGAGAGGATGTCAAGTCAATTAATGTACGCCCCGAGTGCATCAAGTCAA 698  
 Db 626 TGAAGAATTTGGTCCCAATGCCACTGTGGAACCCAGCTGCTGAAGACCAATGAAC 685  
 Qy 699 AATATGATCAAGTCCGAGTTCCACTGGGAACCCAGCAGCAGGAGAGACAGTGAAC 758  
 Db 686 CAGCCCGGGGAGCTCTGCC 704  
 Qy 759 CATCTGGGAGTCTGCC 777

RESULT 5  
 LOCUS AF020502 900 bp mRNA PRI 28-SEP-1997  
 DEFINITION Homo sapiens cytotoxic TRAIL receptor-3 (TRAIL-R3) mRNA, complete cds.  
 ACCESSION AF020502  
 NID g2443819  
 KEYWORDS human.  
 SOURCE  
 ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Vertebrata; Mammalia; Eutheria;  
 Primates; Catarrhini; Hominoidea; Homo.  
 REFERENCE 1 (bases 1 to 900)  
 AUTHORS MacFarlane, M., Ahmad, M., Srinivasula, S.M., Fernandes-Alnemri, T., Cohen, G.M. and Alnemri, E.S.  
 TITLE Identification and Molecular Cloning of Two Novel Receptors for the Cytotoxic ligand TRAIL  
 JOURNAL J. Biol. Chem. (1997) In press  
 REFERENCE 2 (bases 1 to 900)  
 AUTHORS MacFarlane, M., Ahmad, M., Srinivasula, S.M., Fernandes-Alnemri, T., Cohen, G.M. and Alnemri, E.S.  
 TITLE Direct Submission  
 JOURNAL Submitted (21-AUG-1997) Department of Microbiology and Immunology, Kimmel Cancer Institute, 233 S. 10th Street, Philadelphia, PA 19107, USA

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 CDS 1..900  
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 /note="TNFR family member; binds cytotoxic ligand TRAIL; antagonistic decoy receptor, does not contain death domain"  
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 BASE COUNT 228 a 262 c 240 g 170 t  
 ORIGIN

Query Match 18.6%; Score 398; Db 28; Length 900;  
 Best Local Similarity 83.4%; Pred. No. 0.00e+00;  
 Matches 516; Conservative 0; Mismatches 98; Indels 5; Gaps 4;

Db 35 GGAACCTCGGGGACAGCGCGCCCGCCCT-GATGGCGAGGAGGCTGGACCCAGG 93  
 Qy 199 GGAACCTCGGGGACAGCGTCCGACCCGCTCGAGCGCTGAGCAGGCGCTATCCAGG 218  
 Db 94 ACCCAAGACGGGTGGGAACATACCATGCG-CGGATCCCCAGACCTAAAGTCTGT 152  
 Qy 219 AGCAGCAGAGCGTGGGAACAGACATGGCTGTGCGCCCAAGATCTTAAGTCTGT 278  
 Db 153 CGTGTCTATGCTGCGGCTCTGCTGCGAGCTCTACTTACTCTGCGACCATGCCCGCA 212  
 Qy 279 GGTCTTCTATGCTGCGGCTCTGCTGCGGCTCGGTTGACTGTGCAACCATCCCGGCA 338  
 Db 213 GGAGGAAGTTCCTCCAGCAGACAGTGGCCACAGCAACAGAGCAGACAGTTCAGGGGGA 272  
 Qy 339 GGAGGAGTTCCTCCAGCAGACAGTGGCCACAGCAACAGAGCGACGCTCAGGAGGA 398  
 Db 273 GGAGTGTCCAGCAGATCTCATGATCAGACATCTGGAGCTGTAAACCGTGCACAGA 332  
 Qy 399 GGAGTGTCCAGCAGATCTCATGATCAGATATCTGGAGCTGTAAACCGTGCACAGA 458  
 Db 333 GGSTGTGGATACACCAAGGCTTCCACAAATGAACCTCTGTGCTTCCATGTACAGTTTG 392  
 Qy 459 GGSTGTGGATACACCAATGCTTCCACAAATGTGCTTGTGCTGTATGTACAGTTTG 518  
 Db 393 TAAATCAGATCAAAAACATAAAGTTCCTGCACATACAGAGACAGTGTGTCAAGT 452  
 Qy 519 TAAATCAGTCAACAAATAAAGTTCCTGTACACAGCAGAGCAGCTGTGTCAAGT 578  
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 Qy 579 TGAAGAAAGAGCTTCAGGATAAAACATCCCTGAGATGTGCGGAGCTGTAGAACAGG 638  
 Db 511 -TGCCCTAGTGGGAAGTCCAAGTCAATTAATGTACGCTCGGATGATATCAAGTGTGT 569  
 Qy 639 GTGTCCAGAGGATGTCAAGTCAATTAATGTACGCTCGGAGTGTAGATCAAGTCAA 698  
 Db 570 TGAAGAATTTGGTCCCAATGCCACTGTGGAACCCAGCTGCTGAAGACCAATGAAC 629  
 Qy 699 AATATGATCAAGTCCGAGTTCCACTGGGAACCCAGCAGCAGGAGAGACAGTGAAC 758  
 Db 630 CAGCCCGGGGAGCTCTGCC 648  
 Qy 759 CATCTGGGAGTCTGCC 777

RESULT 6  
 LOCUS AF016267 1388 bp mRNA PRI 16-OCT-1997  
 DEFINITION Homo sapiens TRAIL receptor 3 mRNA, complete cds.  
 ACCESSION AF016267  
 NID g2529564  
 KEYWORDS human.  
 SOURCE  
 ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Vertebrata; Mammalia; Eutheria;  
 Primates; Catarrhini; Hominoidea; Homo.  
 REFERENCE 1 (bases 1 to 1388)  
 AUTHORS Schneider, P., Bodmer, J.-L., Thome, M., Holler, N., Hofmann, K. and Tschopp, J.  
 TITLE Characterization of two receptors binding TRAIL  
 JOURNAL FEBS Lett. (1997) In press  
 REFERENCE 2 (bases 1 to 1388)  
 AUTHORS Schneider, P., Bodmer, J.-L., Thome, M., Holler, N., Hofmann, K. and Tschopp, J.  
 TITLE Direct Submission  
 JOURNAL Submitted (28-JUL-1997) Institute of Biochemistry, University of Lausanne, Chemin des Boveresses 155, Epalinges, VD 1066, Switzerland  
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 188. 967  
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 MTRDTVCQCKEGTFRMVNSPEMCRSPGSEGVSNCTSDWDIQCEVEFGANATVE  
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BASE COUNT 331 a 415 c 368 g 274 t  
 ORIGIN

Query Match 18.5%; Score 386; DB 28; Length 1388;  
 Best Local Similarity 83.2%; Pred. No. 0.00e+00;  
 Matches 515; Conservative 0; Mismatches 99; Indels 5; Gaps 4;

Db 102 GGAGCTCTGGGACAGAGGCCCCGGCGGCTGATGGCGGAGCAGGTCGACCCAGG 160

Qy 159 GGGACTTTGGGACAAAGCGTCGCCAGCTCGAGCGCTCGAGAGGGGCTATTCCAGG 218

Db 161 ACCCAGGACGGGTGGGACCACTACCATGG--CCGAGTCCCAAGACCTTAAGTTCGT 219

Qy 219 AGCCAGGACAGCTGGGACCAAGCATGCTCTCTGAGCCCAAGATCTTAAGTTCGT 278

Db 220 GGTGTCATCGTCGGGGTCTCTGTCGAGCTCTTACTCTGCCACACATGCGCCGGA 279

Qy 279 GGTCTTCATCGTCGGGGTCTCTGTCGAGCTCTTACTCTGCCACACATGCGCCGGA 338

Db 280 GGAAGAACTTCCACAGCAGACAGTGGCCCCACAGCAACAGAGCCAGCTTCAGGGGGA 339

Qy 339 GGAAGAACTTCCACAGCAGACAGTGGCCCCACAGCAACAGAGCCAGCTTCAGGGGGA 398

Db 340 GGAGTGTCCAGCAGATCTCATAGATCAGACATATCTGAGCGCTGAACCGCTGCACAGA 399

Qy 399 GGAGTGTCCAGCAGATCTCATAGATCAGACATATCTGAGCGCTGAACCGCTGCACAGA 458

Db 400 GGGTGTGGATTACCAACAGCTCCCAAAATGAACCTCTTGCTCCCAATGACAGTTTG 459

Qy 459 GGGTGTGGATTACCAATGCTCTCCCAAAATGCTCTTGCTCCCAATGACAGTTTG 518

Db 460 TAAATCAGATCAAAACATAAAGTTCTCTGACAGTACACAGACAGCATGTTGTCAGT 519

Qy 519 TAAATCAGTCAAAACATAAAGTTCTCTGACAGTACACAGACAGCATGTTGTCAGT 578

Db 520 TAAAGAGGACACCTTCGGGAATGTTAACTCCACAGAGATGTCGGCGAGTGTAG--CAGG 577

Qy 579 TGAAGAGGAGCTTCCAGATGAAAACTCCCTGAGATGTCGGCGAGTGTAGACAGG 638

Db 578 -TGCCCTAGTGGGAGTCCAAGTCACTAATTTGATGCTCTGGGATGATATCCAGTGTG 636

Qy 639 GTGTCACAGGGGATGTCAGGTCACTAATTTGATGCTCTGGGATGATATCCAGTGTG 698

Db 637 TGAAGAAATTTGGTGCACCTGCTGGAACCCAGCTGCTGAGAGACATGAACAC 696

Qy 699 AATAGATCAGCTGCCAGTTCCATGGGAAACCCACAGCGGAGAGACATGACAC 758

Db 697 CAGCCGGGGATCTTCCCT 715

Qy 759 CATCTGGGGATGCTTGGC 777

RESULT 7  
 LOCUS AF012629 780 bp mRNA PRI 21-AUG-1997

DEFINITION Homo sapiens antagonist decoy receptor for TRAIL/ Apo-2L (TRID)  
 mRNA, complete cds.

ACCESSION AF012629  
 NID 2338430  
 KEYWORDS

SOURCE human.  
 ORGANISM Homo sapiens  
 Eukaryote; mitochondrial eukaryotes; Metazoa; Chordata;  
 Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominoidea;  
 Homo.

REFERENCE 1 (bases 1 to 780)  
 AUTHORS Pan,G., Ni,J., Wei,Y.F., Yu,G., Gentz,R. and Dixit,V.M.  
 TITLE An antagonist decoy receptor and a death domain-containing receptor  
 for TRAIL  
 JOURNAL Science 277 (5327), 815-818 (1997)  
 MEDLINE 97390508

REFERENCE 2 (bases 1 to 780)  
 AUTHORS Pan,G., Ni,J., Wei,Y., Yu,G., Gentz,R. and Dixit,V.M.  
 TITLE Direct Submission  
 JOURNAL Submitted (06-JUL-1997) Pathology, University of Michigan, 1301  
 Catherine Road, Room 7518, Ann Arbor, MI 48109, USA

FEATURES  
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 /gene="TRID"  
 CDS 1. 780  
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BASE COUNT 202 a 226 c 196 g 156 t  
 ORIGIN

Query Match 16.6%; Score 345; DB 28; Length 780;  
 Best Local Similarity 84.6%; Pred. No. 1.22e-273;  
 Matches 440; Conservative 0; Mismatches 77; Indels 3; Gaps 2;

Db 12 CCCCAGACCTTAAGTGTGTCGTGTCATGTCGGCGGTCTGTCGCGCATCTAGCTTA 71

Qy 258 CCCCAGATCTTTAGTGTGTCGTGTCATGTCGGCGGTCTGTCGCGCATCTAGCTTA 317

Db 72 CTCTGCCACACCTGCCCGCAGAGGAGTTCCTCCAGCAGATGCGCCACAGCAGCA 131

Qy 318 CTCTGCCACACCTGCCCGCAGAGGAGTTCCTCCAGCAGATGCGCCACAGCAGCA 377

Db 132 GAGGCGACCTTCAAGGGGAGGAGTTCGACAGATCTCATGATCAGACATCTAG 191

Qy 378 GAGGCGAGCTTCAAGGGGAGGAGTTCGACAGATCTCATGATCAGACATCTAG 437

Db 192 AGCCTGTAAACCGTGCACAGAGGAGTGGATACCAACGCTTCCACATGAACTTC 251

Qy 438 AGCCTGTAAACCGTGCACAGAGGAGTGGATACCAACGCTTCCACATGAACTTC 497

Db 252 TTGCTTCCCATGTACAGTTTGAATCAGATCAAAACATAAAGTTCTGACCATGAC 311

Qy 498 TTGCTTCAATGATACAGTTTGAATCAGATCAAAACATAAAGTTCTGACCATGAC 557

Db 312 CAGAGACAGATGTCGATGTAAGTAAGGAGACCTTCGGAGATGAAACTCCCCAGAT 371

Qy 558 CAGAGACAGCTGTCGATGTAAGTAAGGAGACCTTCGGAGATGAAACTCCCCAGAT 617

Db 372 GTGCCGAGGTAG--CAGG-TGCCCTAGTGGGAGTCCAAGTCAGTATTTGACGTC 428

Qy 618 GTGCCGAGGTAGAGAGGAGTGTCCAGAGGAGTGTCAAGTCAGTATTTGACGTC 677

Db 429 CTGGGATGATATCAAGTGTGTTGAAGAAATTTGGTGCACCTGACCTGTGAAACCCAGC 488

Qy 678 CCGAGTGCATCAAGTCAAAATGATCAGTCGACCTGACCTGCGGAGAAACCCAGC 737

Db 489 TCGTGAAGACATGAACACACCGCCGGGAGCTCTCC 528

Qy 738 AGCGAGGAGACAGTACCCACCATCTCTGGAGTGTGCC 777

RESULT 8  
 LOCUS AF018658 1323 bp mRNA PRI 18-SEP-1997  
 DEFINITION Homo sapiens apoptosis inducing protein (TRICK2B) mRNA, complete cds.  
 ACCESSION AF018658  
 NID g2407652  
 KEYWORDS  
 SOURCE human.  
 ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Vertebrata; Mammalia; Eutheria;  
 Primates; Catarrhini; Hominoidea; Homo.  
 REFERENCE 1 (bases 1 to 1323)  
 AUTHORS Screaton,G.R., Mongkolsapaya,J., Xu,X., Cowper,A.E., McMichael,A.J. and Bell,A.J.  
 TITLE TRICK2 a new alternatively spliced receptor which transduces the cytotoxic signal from TRAIL  
 JOURNAL Curr. Biol. (1997) In press  
 REFERENCE 2 (bases 1 to 1323)  
 AUTHORS Screaton,G.R., Mongkolsapaya,J., Xu,X., Cowper,A.E., McMichael,A.J. and Bell,A.J.  
 TITLE Direct Submission  
 JOURNAL Submitted (12-AUG-1997) Molecular Immunology, Institute of Molecular Medicine, Oxford University, John Radcliffe Hospital, Headington, Oxford OX3 9DS, UK  
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 CDS 1. 1323  
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 BASE COUNT 319 a 343 c 397 g 264 t  
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Query Match 12.7%; Score 264; DB 28; Length 1323;  
 Best Local Similarity 68.6%; Pred. No. 3.16e-200;  
 Matches 705; Conservative 1; Mismatches 298; Indels 24; Gaps 17;

Db 1 ATGGAAACAGGGGACAGAACGCCCGCGCTCTGGGGGCGGAGGAGCGACGCCA 60  
 Qy 157 ATGGACATTGGGACAAAGCGTCCGACCCCTCGAGCGCTGACGAGGGGCTATCCA 216  
 Db 61 GGACCCAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 118  
 Qy 217 GGAGCCAGGACAGCGTCCGGAAACGACACATGGCTCTGGACCCCAAGATCTTAA 276  
 Db 119 -TCG--TG-TCCGCGCGGCTCTGCTGGTGTCTCAGCTGAGTCTGCTGATCAACCA 174  
 Qy 277 GTGCTTCATCATCTCGCGGTCTCTGCTGCGGTCCGGGTGACTCTGCCACATCCCCG 336  
 Db 175 CAAGACTAGTCCCGACGAGAGGTGGCCCAACAAAGAGGTCCAGCCCTCAGAG 234

Qy 337 CAGGACGAAGTCTCCCGACGACAGTGGCGCCACGACAGGAGGCGAGCTCAGAG 396  
 Db 235 GATTGTGTCTACCTGGACACCATATCTCAGAGAGGATGAGATGTCTCTCTCAA 294  
 Qy 397 GAGGAGTGTCCAGCAGGATCTCATAGTCAGATATCTAGGCGCTGTAAACCGTGACA 456  
 Db 295 TATGACGAGCATATAGCATCTCAGTCACTGGTGAATGACCTTTTCTGCTGGCTCACCAG 354  
 Qy 457 GAGGCTGTGGATACCAATGCTTCCACAAATTTGCTCTTCTGCTGTATGTACAGTT 516  
 Db 355 TGTGATTAGTGAAGTGGAGTAACTGCTCCCTGACACGACGACGACACAGTGTGAC 414  
 Qy 517 TGTAAATCAGTCAACAAATAAAGTCTCTGCTACACGACGACGACGACGAGTGTGAC 576  
 Db 415 TGCAGGAAGGACCTTCCGGGAGAGATTTCTCTGAGATGTGCGGAGTGGCCGACA 474  
 Qy 577 TGTCAAAAGGAGCTCCAGGATAAACTCCCTGAGATGTGCGGAGTGTGAGAAC 636  
 Db 475 GGGTGTCCGAGGAGGTGTCAAGTGTGCTGATGTACACCTGGAGTGTGATGTGATGT 534  
 Qy 637 GGGTGTCCGAGGAGGTGTCAAGTGTGATGTATGTAGCCCGGAGTGTGATGTGATGT 694  
 Db 535 GTCCCAAGATCAGGTACAAACAGACATGGGAGGCCCGAGTGTGGAGGAGAGGTG 594  
 Qy 695 G-CAAAATGATCAGTCCGAGTCTCCGAGTGTGAGGAGGAGGAGGAGGAGTGTG 753  
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 Qy 814 GTCACTATTTTAACTGTGTTGTGTTGTGTTTTCATGTGAGAGAAATTCATTTTAC 873  
 Db 711 GAAGAAAGTCTCTCTTACCTGAAG-GCATCTCTCAGTGTGGTGTGGG-GACCTGAG 768  
 Qy 874 CTCAGAGGATCTCTCAGTGTGGTGAAGAGTCCGAGGAGTGTGACAGAGTCTTTTC 933  
 Db 769 CGTGTG-GA-CAGAGCT-CACACGACCTGGGGTGGAGCAATGTCTCAATGAGATC 825  
 Qy 934 CGCGCGCTCATGTCTTCTCAGAGTCTCTGCGGCGAGGACATGCCGCAACGAGCC 993  
 Db 826 GTAGTA-----T-CTTCCAGGCCACCGAGTCTCTGAGCAGGAATGGAAGTCAAGAG 879  
 Qy 994 CTGACTACAGATCTTCCAGCCGCCAGGCTCTCTGAGCAGGAATCAAGGTCAAGAG 1053  
 Db 880 CCAGCAGAGCCAAAGGTGTCAACATGTGTCCCGGGGAGTCAAGAGATCTCTGTGAA 939  
 Qy 1054 CTGGCAGAGCTACAGGTGTGACTGTAGATGTGAGAGGAGCCAGGCTCTCTGTGAA 1113  
 Db 940 CCGGCAAGAGCTGAAAGGTCTCAGAGGAGGAGGCTGTGGTTCAGCAATGAAGGTAT 999  
 Qy 1114 CAGCAGAGGCTGAAGGAGTGTGAGAGGAGGAGGCTGTGGTTCAGTGAATGACCTGAC 1173  
 Db 1000 CCACTGA 1007  
 Qy 1174 TCCCTGA 1181

RESULT 9  
 LOCUS AF016266 3993 bp mRNA PRI 16-OCT-1997  
 DEFINITION Homo sapiens TRAIL receptor 2 mRNA, complete cds.  
 ACCESSION AF016266  
 NID g2529562  
 KEYWORDS  
 SOURCE human.  
 ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Vertebrata; Mammalia; Eutheria;  
 Primates; Catarrhini; Hominoidea; Homo.  
 REFERENCE 1 (bases 1 to 3993)  
 AUTHORS Schneider,P., Bodmer,J.-L., Thome,M., Holler,N., Hofmann,K. and



TITLE Tschopp,J.  
 JOURNAL Characterization of two receptors binding TRAIL  
 FEBS Lett. (1997) In press  
 REFERENCE 2 (bases 1 to 3993)  
 AUTHORS Schneider,P., Bodmer,J.-L., Thome,M., Holler,N., Hofmann,K. and Tschopp,J.  
 TITLE Direct Submission  
 JOURNAL Submitted (28-JUL-1997) Institute of Biochemistry, University of Lausanne, Chemin des Boveresses 155, Epalinges, VD 1066, Switzerland  
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 118..1440  
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 /note="DR4 homolog; contains a death domain similar to TNF receptor; TRAIL receptor 2 has been mapped by linkage to STS WI-1701 to human chromosome 8, to locus 8p12-21"  
 /codon\_start=1  
 /product="TRAIL receptor 2"  
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 BASE COUNT 961 a 964 c 1014 g 1052 t 2 others  
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 Query Match 12.7%; Score 265; DB 28; Length 3993;  
 Best Local Similarity 68.6%; Pred. No. 3.97e-201;  
 Matches 706; Conservative 1; Mismatches 298; Indels 24; Gaps 17;

Db 117 CATGGAACAAGCGGGACAGAACGCCCGCCGCTTGGGGGCGGGAAAGCAGGGGCC 176  
 Qy 156 CATGGAGCTTTGGGGAACAAGCGTCCCGACCGCTCGAGCGTCTGAGCAGGGCGTATCC 215  
 Db 177 AGGACCCAGGAGGCGGGGAGGACCGAGCGTGGCGTCCGGTCCCAAGACCTT- GTG 234  
 Qy 216 AGGAGCCAGGACAGCGTGGGGAACCAACACATGCTCTCGACCCACAGATCCTTAAGTT 275  
 Db 235 C-TGCT- TG-TGCGCGGCTGCTGCTGTGGTCTCAGTGAGTCTGCTGTATCACCA 290  
 Qy 276 CGTGCTCTCTCACTGTCGGGTCTCTGCGCGTCCGGGTGACTCTGCCACATCCCCCG 335  
 Db 291 ACAAGACTAGCTCCCGACAGAGAGTGGCCCCACAACAAGAGGCTCAGCGCCCTCAGA 350  
 Qy 336 CGAGGACAAAGTTCCTCCACAGACAGTGGCCCCACAGACAGAGGCGACGCTCAAGGA 395  
 Db 351 GGGATGTGTGCTCACTGGACACCATATCTCAGAGACGGTACAGATGCATCTCTCGAA 410  
 Qy 396 GGAGGAGTGTCCAGCAGGATCTCATAGATCAGATATATCTGAAGCTGTATACCCGTGAC 455  
 Db 411 ATATGACAGGACATAGACACTCACTGGAATGACCTCTTTCTGCTGGCGTGACACG 470  
 Qy 456 AGAGGCTGTGATTACACCATGCTCTCCACAAATGTCTGCTTGTGCTGATGTACAGT 515  
 Db 471 GTGTGATTAGGTGAAGTGAGCTAAGTCTGCTGCCACAGCAGAGAACAGATGTGTCA 530  
 Qy 516 TTGTAAATCAGGTCAACAATAAAGATTCTGTACACAGACAGACACCGTGTGTCA 575  
 Db 531 GTGGGAAGAGGCACCTTCCGGGAAGAAGATTCTCTGAGATGTGCGGAAGTGGCGAC 590  
 Qy 576 GTGTGAAGAGGAGCTCCAGGATAAAGATCTCCCTGAGATGTGCGGAGTGTAGAAC 635  
 Db 591 AGGGTGTCCCAAGGGATGGTCAAGGTGCGTGATTGTACAGCTCCGAGTGACATGAGT 650

Qy 636 AGGGTGTCCCAAGGGATGGTCAAGGTCAAGTATTGTATGACCCCGAGTGACATC-AA-G 693  
 Db 651 TGTCACAAGAATCAGTCAAGACAGTGGGGAGCCCGAGCTGTGGAGGAGACGGT 710  
 Qy 694 TG-CAAAAATGAATCAGTCCAGTTCACGTGGGAAACCCACAGCAGCGGAGGACAGT 752  
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 Qy 753 GACCAACATCTCGGGATGCTGTCTCTCCCTATCACTACCTTATCATATAGTGGTTTT 812  
 Db 768 AGTCACAGTTCAGCGCTAGTCTGATTGTGGCTGTGTT-GTTTCAAGTCTTACTGT 826  
 Qy 813 AGTCATCATTTTACGTCTGGTGTGTGGTGGCTTTTCATGTGCGAAGAAATTCATTCTTA 872  
 Db 827 GGAAGAAATCTCTTCTTACCTGAAG-GCATCTCTCAGTGGTGGTGGG-GAOCCTGA 884  
 Qy 873 CCTCAAGGCATCTGCTCAGTGGTGGAGGAGTCCCGAAGCTGTGCACAGATCTCTTT 932  
 Db 885 GCGTGTG-GA-CAGAGCT-CACAGACAGTGGGCTGAGGACATGTCTCAATGAGAT 941  
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 Db 942 CGTAGTA- ----T-CTTGACGCCACCGAGCTCTGACGAGAAATGGAAGTCCAGGA 995  
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 Db 1056 ACCCGCAGAGCTGAAGAGTCTCAGACAGAGAGCTGCTGTGTCAGCAATGAGGTGA 1115  
 Qy 1113 ACAGGACAGAGCTGAAGGGTGTACAGAGAGAGGCTCTGTGTCAGTGAATGAGCTGA 1172  
 Db 1116 TCCACTGA 1124  
 Qy 1173 CTCCTGCTGA 1181  
 RESULT 10  
 LOCUS AF016849 1859 bp mRNA PRI 07-OCT-1997  
 DEFINITION Homo sapiens apoptosis inducing receptor TRAIL-R2 (TRAILR2) mRNA, complete cds.  
 ACCESSION AF016849  
 NID g2465585  
 KEYWORDS  
 SOURCE human.  
 ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 REFERENCE 1 (bases 1 to 1859)  
 AUTHORS Walczak,H., Degli-Esposti,M.A., Johnson,R.S., Smolak,P.J., Waugh,J.T., Bolani,M., Timour,M.S., Gerhart,M.J., Schooley,K.A., Smith,C.A., Goodwin,R.G. and Rauch,C.T.  
 TITLE TRAIL-R2: a novel apoptosis-mediating receptor for TRAIL  
 JOURNAL EMBO J. 16 (17), 5386-5397 (1997)  
 MEDLINE 97459925  
 REFERENCE 2 (bases 1 to 1859)  
 AUTHORS Walczak,H.  
 TITLE Direct Submission  
 JOURNAL Submitted (31-JUL-1997) Immunobiology, Immunex Corp., 51 University St., Seattle, WA 98101, USA  
 FEATURES  
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 /gene="TRAILR2"  
 CDS 145..1467

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BASE COUNT 458 a 471 c 511 g 419 t  
 ORIGIN

Query Match 12.4%; Score 259; DB 28; Length 1859;  
 Best Local Similarity 68.3%; Pred. No. 1.01e-195;  
 Matches 703; Conservative 1; Mismatches 301; Indels 24; Gaps 17;

Db 144 CATGGAAACAAGGGGACAGAAAGCCCGGCCGCTTCGGGGGCGGAAAAGACAGGCGCC 203  
 Qy 156 CATGGGACTTTGGGACAAAGCGTCCGACGCCCTCGAGCGCTGAGACGGGCGTATCC 215

Db 204 AGGACACAGGAGCGCCCGGGAGCAGCGCTGGCGCCGGGCTCCCAAGACCTT-6TG 261  
 Qy 216 AGGACACAGGAGCGCGGGAACAGACCCATGGCTCGAGCCCAAGATCTCTTAAGTT 275

Db 262 C-TGT-TG-TGCGCGGGGTCTGCTGTGTGGCTCAGCTGAGTCTGCTCATACCCA 317  
 Qy 276 GTGTGCTTCATCTGTCGGGTCTGCTGCGGGCGGGGTGACTCTGCCACATCCCGCG 335

Db 318 ACAAGACCTAGCTCCCAAGACAGAGCGGCCCCACAAAGAGAGTCCAGCCCTCAGA 377  
 Qy 336 GCAGGACAGAGTTCCCAAGACAGAGTGGGCCACAGCAGACAGAGCGGAGCTCAAGGA 395

Db 378 GGGATTGTGTCCACTGGACACCATATCTCAGAAGCGGTAGAGATTGCTATCTCCGAA 437  
 Qy 396 GGGAGAGTGTCCAGCAGATCTCATAGATCAGATATATCTGGAGCGTGAACCGCTGAC 455

Db 438 ATATGGACAGCATTAGCATTCTGAGTACCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 497  
 Qy 456 AGAGGCTGTGGATTACACCATTTGCTCCAACTTGTCTGCTGCTGCTGCTGCTGCTGCT 515

Db 498 GTGTATTCAAGTGAAGTGAGCTAAGTCTGCACACAGCAGAGAAACAGTGTGTCA 557  
 Qy 516 TTGTAAATCAGTCAAAACAAATAAAGTTCTGTGACACAGCAGACACCTGTGTCA 575

Db 558 GTGGAAGAAGGCACTTCGGGAAGAAGATTCTCTGAGATGTGCGGGAAGTGGCGAC 617  
 Qy 576 GTGTGAAAAGGAAGCTCCAGAGTAAATAAATCCCTGAGATGTGCGGAGCTGTAGAC 635

Db 618 AGGGTGTCCAGAGGATGTCAAGTGTGCTGATTTGTATCAGCTGGAGTACATGGAATG 677  
 Qy 636 AGGGTGTCCAGAGGATGTCAAGTGTGATTAATTTATGAGCCGGAGTCAATC-AA-6 693

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Db 854 GGAAGAAAGTCTCTTACTGAAAG-GCATCTGTGAGTGTGTGTGTGTGTGTGTGTGTGT 911  
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Db 912 GCGTGTG-GA-CAGAAGT-CACACGACCTGGGCTGAGGCAATGCTCTCAATGAGAT 968  
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Db 969 COTGAGTA-----T-CTTGACGCCACCCAGGCTCCTGAGCAGGAATGGAAGTCAGGA 1022  
 Qy 993 CCTGAGTACAGATCTCTGACGCCACCCAGGCTCTGAGCAGGAATCAAGGTCAGGA 1052

Db 1023 GCACGACGAGCCACAGGTGTCAACATGTGTCCCGCGGGAGTCAAGCATCTCTGGA 1082  
 Qy 1053 GCTGCGGACATCAAGGTGTGACTGTAGATGTGACGAGGAGCCACAGGTCTCTGGA 1112

Db 1083 ACCGCGAGAAGCTGAAGGTCTCAGAGGAGAGGCTGCTGTGCTCCAGCAATGAAGTGA 1142  
 Qy 1113 ACAGGACAGAAGCTGAAGGCTGTGAGAGGAGAGGCTGCTGTGCTCCAGTGAATGACGTGA 1172

Db 1143 TCCCTAGTA 1151  
 Qy 1173 CTCCTGTA 1181

RESULT 11  
 LOCUS HSU90875 1407 bp mRNA PRI 19-APR-1997

DEFINITION Human cytotoxic ligand TRAIL receptor mRNA, complete cds.  
 ACCESSION U90875  
 NID g1945071  
 KEYWORDS  
 SOURCE human.  
 ORGANISM Homo sapiens  
 Eukaryote; mitochondrial eukaryotes; Metazoa; Chordata; Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.

REFERENCE 1 (bases 1 to 1407)  
 AUTHORS Pan,G., O'Rourke,K., Chinaiyan,A.M., Gentz,R., Ebner,R., Ni,J. and Dixit,V.M.  
 TITLE The receptor for the cytotoxic ligand TRAIL  
 JOURNAL Science 276 (5309), 111-113 (1997)  
 MEDLINE 97238921

REFERENCE 2 (bases 1 to 1407)  
 AUTHORS Pan,G., O'Rourke,K., Chinaiyan,A.M., Gentz,R., Ebner,R., Ni,J. and Dixit,V.M.  
 TITLE Direct Submission  
 JOURNAL Submitted (25-FEB-1997) Pathology, University of Michigan, 1301 Catherine Road, Ann Arbor, MI 48109, USA

FEATURES  
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BASE COUNT 328 a 355 c 434 g 290 t  
 ORIGIN

Query Match 9.7%; Score 202; DB 28; Length 1407;  
 Best Local Similarity 78.7%; Pred. No. 1.05e-144;  
 Matches 277; Conservative 0; Mismatches 75; Indels 0; Gaps 0;

Db 335 ACCTCATGATCAATCAATTTGGCAGACAGTGGGAACAGCCCTTTGGGAGAGTGT 394  
 Qy 344 AGGTTCCCGACAGCAGTGGTCCCGACAGCAACAGAGGCGCAGCCTCAGGAGGAGAGT 403

Db 395 GTCCACAGGATCTCATAGATCAGAACGTCCTGGAGCCTGTAAACCGGTGCACAGGGTG 454  
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 Qy 404 GTCCACAGGATCTCATAGATCAGAAATATCTGGAGCCTGTAAACCGGTGCACAGGGTG 463  
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 Db 575 CAGGACTTCTCCGAGTCAAGTCTGTCTGAGATGTGCGGAGTGTGAGCAGAGGTGCC 634  
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 Qy 584 AAGGAGCTTCCGAGTCAAAATCTCCCTGAGATGTGCGGAGTGTGAGACAGGTGTCT 643  
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 Qy 644 CCAGAGGGATGGTCAAGGTCAAGTATGTAGCCCTGGAGTGACATCAAGTG 695  
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RESULT 12  
 LOCUS AF020501 1236 bp mRNA PRI 28-SEP-1997

DEFINITION Homo sapiens cytotoxic TRAIL receptor-2 (DR5) mRNA, complete cds.  
 ACCESSION AF020501  
 NID g2443817  
 KEYWORDS  
 SOURCE human.  
 ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Vertebrata; Mammalia; Eutheria;  
 Primates; Catarrhini; Hominoidea; Homo.  
 1 (bases 1 to 1236)  
 REFERENCE  
 AUTHORS MacFarlane,M., Ahmad,M., Srinivasula,S.M., Fernandes-Alnemri,T.,  
 Cohen,G.M. and Alnemri,E.S.  
 TITLE Identification and Molecular Cloning of Two Novel Receptors for the  
 Cytotoxic ligand TRAIL  
 J. Biol. Chem. (1997) In press  
 2 (bases 1 to 1236)  
 REFERENCE  
 AUTHORS MacFarlane,M., Ahmad,M., Srinivasula,S.M., Fernandes-Alnemri,T.,  
 Cohen,G.M. and Alnemri,E.S.  
 TITLE Direct Submission  
 JOURNAL Submitted (21-AUG-1997) Department of Microbiology and Immunology,  
 Kimmel Cancer Institute, 233 S. 10th Street, Philadelphia, PA  
 19107, USA

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 CDS 1. 1236  
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 GSEHLLPEAERSSQRRLVLPANEGDPTETLRQCTDPAFLVPTDSWEPLMKRLGL  
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BASE COUNT 302 a 314 c 372 g 248 t

Query Match 9.44; Score 195; DB 28; Length 1236;  
 Best Local Similarity 70.94; Pred. No. 1.75e-138;

Matches 382; Conservative 0; Mismatches 151; Indels 6; Gaps 4;

Db 1 ATGGAACAACGGGACAGAACGCCCGGCCCTGTGGGGGCGGGAAGGACGCGCCA 60  
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 Db 61 GGACCCAGAGGGGAGGGGAGCCAGGCTGGCTCGGGTCCCCAAGACCCCTT-CTGC 118  
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 Qy 217 GGAGCCAGAGCAGCTCGGGAACAGACCATGGCTCTGGACCCCAAGATCTTAACTTC 276  
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 Db 119 -TCGT--TG-TCGCCGCGCTGCTGTGTGGTCTCAAGTAGTCTGTCTGATCAACCA 174  
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 Qy 277 GTGCTCTTCATCGTCGGTCTGTCTGCCGCTCGGTTGACTGTGCCACATCCCCGG 336  
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 Db 175 CAGAGCTAGTCCCGCAGCAGAGTGGCCCAACACAAAGAGTCCAGCCCTCAGAG 234  
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 Qy 397 GAGAGTGTCCACAGGATCTCATGATCAGATATCTTGGAGCTGTACCGCTGCA 456  
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 Qy 577 TGTGAAAAGAGACCTTCAGGATAAATCTCCCTGAGATGTCCCGAGCTGTGAGACA 636  
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RESULT 13  
 LOCUS AF018657 1236 bp mRNA PRI 18-SEP-1997

DEFINITION Homo sapiens apoptosis inducing protein (TRICK2A) mRNA, complete cds.  
 ACCESSION AF018657  
 NID g2407650  
 KEYWORDS  
 SOURCE human.  
 ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Vertebrata; Mammalia; Eutheria;  
 Primates; Catarrhini; Hominoidea; Homo.  
 1 (bases 1 to 1236)  
 REFERENCE  
 AUTHORS Screaton,G.R., Mongkolsapaya,J., Xu,X., Cowper,A.E., McMichael,A.J.  
 and Bell,A.J.  
 TITLE TRICK2 a new alternatively spliced receptor which transduces the  
 cytotoxic signal from TRAIL  
 JOURNAL Curr. Biol. (1997) In press  
 2 (bases 1 to 1236)  
 REFERENCE  
 AUTHORS Screaton,G.R., Mongkolsapaya,J., Xu,X., Cowper,A.E., McMichael,A.J.  
 and Bell,A.J.  
 TITLE Direct Submission  
 JOURNAL Submitted (12-AUG-1997) Molecular Immunology, Institute of  
 Molecular Medicine, Oxford University, John Radcliffe Hospital,  
 Headington, Oxford OX3 9DS, UK

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 CDS 1. 1236  
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 CSGGGGDPFVRDSSQRPAEDVNLNIVSLIQTPVPEMEVPEAETGVNMLSP  
 GESEHLLPEAERASQRRLIVANEGDPTETLRQCFDFAVLVFDSEWELMKLGL  
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BASE COUNT 302 a 314 c 372 g 248 t  
 ORIGIN

Query Match 9.4%; Score 195; DB 28; Length 1216;  
 Best Local Similarity 70.9%; Pred. No. 1.75e-136;  
 Matches 382; Conservative 0; Mismatches 151; Indels 6; Gaps 4;

Db 1 ATGGAAACACGGGACAGAACGCCCGCGCTCTGGGGGCGCGAAAGGACGAGGCCA 60

Qy 157 ATGGGACTTTGGGGAACAAAGCTCCGACGCCCTCGAGCTCGAGCAGGGCGTATCCA 216

Db 61 GGACCCAGGAGGCGGGGAGGACGAGGCTGGGCTCGGGTCCCAAGACACCTT -GTGC 118

Qy 217 GGAGCCAGGACAGGCTGGGAAACGACACCTGCTTGGACCCAGAGCTTTTAGTTC 276

Db 119 -TCGT--TG-TGCCCGCGGTCTGCTGTGTGGTCTCAGCTAGCTGTCTGATCACCCA 174

Qy 277 GTCGTCTTCACTGTCGGGCTCTGCTGCGGGTGGGTGACTCTGCACCACTCCCGCG 336

Db 175 CAGAGCTAGCTCCCGCAGAGAGTGCCGCCACCAAAAGAGTCCACGCCCTCAGAG 234

Qy 337 CAGGACGAGTTCGCCAGCAGACAGTGCCGCCACACAGAGGCGCAGGCTCAGAGAG 396

Db 235 GGATGTGTCCACTGGACACCATATCTCAGAGAGCGTAGAGTTGCACTTCTCTGCAA 294

Qy 397 GAGGAGTGTCCAGGAGTCTCATAGATCAGATATCTAGAGGCTGTACACCGTGACA 456

Db 295 TATGGACAGGACTATAGCACTCAGTGAATGACCTCTTCTTCTGCTGCGCTGCACAG 354

Qy 457 GAGGCTGTGATACACCATTCCTTCCACAAATTTGCTCTTCTGCTGATGACAGTT 516

Db 355 TGTGATTCAGGTGAAGTGAGCTAAGTCCGTGCACACGACCAAGAACACATGTGTGAC 414

Qy 517 TGTAAATCAGGTCAAAACAATAAAGTTCTCTGTACACGACGACAGACAGCTGTGTGAC 576

Db 415 TGGGAAGAAGGACCTTCGGGGAAGAGATTCTCTGAGATGTGGCGGAAGTGCGCGACA 474

Qy 577 TGTGAAGAAGAAGCTTCAGGATAAAATTCCTCTGAGATGTGGCGGAGCTGTAGACA 636

Db 475 GGGTGTCCAGAGGAGTGTCAAGTGGTGAATGTACACCTGGAGTGACATGCAATG 533

Qy 637 GGGTGTCCAGAGGAGTGTCAAGTGAATGTGAATGTACACCTGGAGTGACATGCAATG 695

RESULT 14  
 LOCUS AF016268 1717 bp mRNA PRI 05-FEB-1998

DEFINITION Homo sapiens death receptor 5 (DR5) mRNA, complete cds.

ACCESSION AF016268

NID g2832229

KEYWORDS

SOURCE human.

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Vertebrata; Mammalia; Eutheria;

Primates; Catarrhini; Hominoidea; Homo.

REFERENCE 1 (bases 1 to 1717)

AUTHORS Chaudhary,P.M., Eby,M., Jasmin,A., Bookwalter,A., Murray,J. and

Hood,L.

TITLE Death receptor 5, a new member of the TNF family, and DR4 induce

FADD-dependent apoptosis and activate the NF-kappaB pathway

JOURNAL Immunity 7 (6), 821-830 (1997)

MEDLINE 98090092  
 REFERENCE 2 (bases 1 to 1717)  
 AUTHORS Chaudhary,P.M., Eby,M., Jasmin,A., Bookwalter,A. and Hood,L.  
 TITLE Direct Submission  
 JOURNAL Submitted (28-JUL-1997) Molecular Biotechnology, University of  
 Washington, NE Pacific Street, Box 357730, Seattle, WA 98195-7730,  
 USA

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 NF-kappa B pathway"  
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BASE COUNT 437 a 425 c 467 g 388 t  
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Query Match 9.4%; Score 196; DB 28; Length 1717;  
 Best Local Similarity 70.9%; Pred. No. 2.27e-139;  
 Matches 383; Conservative 0; Mismatches 151; Indels 6; Gaps 4;

Db 109 CATGGAAACACGGGACAGAACGCCCGCGCTCTGGGGGCGCGAAAGGACAGGGCCC 168

Qy 156 CATGGGACTTTGGGGAACAAAGCTCCGACGCCCTCGAGGCTCGAGCGGGCGCTATCTC 215

Db 169 AGGACCCAGGAGGCGCGGGGACCGAGCGTGGCTCGGGTCCCAAGACCTTT -GTG 226

Qy 216 AGGAGCCAGGACAGCTCGGGGACACAGCATAGCTCTGGACCCAGATCTTAAGTT 275

Db 227 C-TGCT--TG-TGCCCGCGGTCTGCTGTGTGGTCTCAGCTAGCTGTCTGATCACCCA 282

Qy 276 CTTGCTCTTCATGTCGCGGCTCTGCTGCGCGTCCGGGTGACTCTGCCACATCCCTCCG 335

Db 283 ACAAGACCTAGTCCCAAGCAGAGAGTGCGCCCAACAAGAGGATCCAGCCCTCAGA 342

Qy 336 CGAGGACGAAGTTCCCAAGCAGAGAGTGCGCCCAAGCAGAGGCGGCGCATCTCAAGA 395

Db 343 GGGATGTGTCCACTGGACACCATATCTCAGAAAGCGGTAGAGATTGCACTCTCTGCAA 402

Qy 396 GGAGGAGTGTCCAGGAGTCTCATAGATCAGAAATATCTGAGGCTGTAAACCGTGAC 455

Db 403 ATATGGACAGGACTATAGCACTCACTGGAATGACCTCTTTCTGCTGCGGTGCACAG 462

Qy 456 AGAGGTGTGGATACACATCTGCTTCCACAAATTTGCTCTTCTGCTCTATGACAGT 515

Db 463 GTGTGATTCAGGTGAAGTGGAGCTAAGTCCCTGCACACGACCAAGACAGTGTGTCA 522

Qy 516 TTGTAAATCAGGTCAACAAATAAAGTCTCTGTACACGACCAAGACAGCTGTGTCA 575

Db 523 GTGGGAAGAAGGACCTTCGGGGAAGAGATTCTCTAGATGTGCGGAGTGCCGCAC 582

Qy 576 GTGTGAAGAAGAAGCTTCCAGGATAAAATCTCCCTGAGATGTGCGGAGCTGTAGAAC 635

Db 583 AGGGTGTCCAGAGGAGTGTCAAGTGGTGTGATTTGTCACCCGAGTGCATGATGATG 642

Qy 636 AGGGTGTCCAGAGGAGTGTCAAGTGAAGTAAATTTGTCACCCGAGTGCATCAAGTG 695



Db	1	MEGRQQAISGAKRHQPGFPREARGPGLRVYPTLVIVL--AAVLVLGAESALITQ	58
Qy	1	MEGLQSGVPTASSARGFRAGRTASTGRLDWLDPKLVFPVIVLVLVWVDSATIPR	60
Db	59	QDLAPQVAPQPKKSPSEGLCPGHHISEDRDRCISCKYQDYTSIWNDLLECLFCTR	118
Qy	61	QDEVFOQTVAQQKRSLEKECPAGSHREYTGACNCTBEGVDYTIASNNPLSCLLTV	120
Db	119	CDSEGVLELSPCTTTRMTVQCCEGTFREEDSPMCKRCPCTPGMVKVYGDCTPWSIDC	178
Qy	121	CKSQNTWSSCTTTRDTVQCCKGSPDKNSPMCKRTRCPCTPGMVKVWCTSPDIKC	180
Db	179	VHREKSTKHSGAPAAVEETVTSPTQSPASCSLGIIGTVAAVLVLVAVFCVCSLLAK	238



Db 1 MEDGQNPAPASGAKRHGHPGPPREAGAR...-GFVPTKTVLVVAALLVLSAESALT 57  
Qy 1 MGLNGQSVPTASASGAKRHGHPGPPREAGAR...-GFVPTKTVLVVAALLVLSAESALT 57

Db 58 QDQLAPQQAAPQKRSRSPSGKPPGHHISDGRCKISCKYQDQSTHWNLLDLCLRCT 117  
Qy 60 RQDEVQQTVAPOQRKSRSLKSEPCAGSHRSSTTGACNCTGDEVDTIASNMLSCLLCT 119

Db 118 RCDSGHVELSPCTTTRNTWCQEHGSTRFEEDSPMCNCRKRTGCPGHWKVDCTPWSDIE 177  
Qy 120 VCKSGQKMSSTCTTTRNTWCQEHGSTRFEEDSPMCNCRKRTGCPGHWKVDCTPWSDIE 177

Db 178 CVR...K...T...FSGI...ILGV...T...VAANVLVA-PWCKSL-PPKSLPV 214



Yq 180 CNKSAASSTGKTAAEETVTTILGLASPYHYLIIVLVILAAVVGFSCKRKFISY 239  
 Db 215 LKGCISGGGGDPKVRD---SSQ-R-PGAEDNVLNEIVSI--LQTPVPEQEMEVQE 264  
 Yq 240 LKGCISGGGGGPKVRHVLFRRCSPSRVPGAEDNARNETLSNRLQTPVSEQIQOE 299

Db 265 PAEPTGVNMLSPGESEHLLEPAEAERQRRRLVPANEGDPT 307  
 Yq 300 LAELTGVTXPEEPQRLLEQAEAGCQRRRLVPVNDASD 342

RESULT 8  
 ID 000220 PRELIMINARY; PRT; 468 AA.

AC 000220;  
 DT 01-JUL-1997 (TREMBLREL. 04, CREATED)  
 DT 01-JUL-1997 (TREMBLREL. 04, LAST SEQUENCE UPDATE)  
 DT 01-JAN-1998 (TREMBLREL. 05, LAST ANNOTATION UPDATE)  
 DE CYTOTOXIC LIGAND RECEPTOR.  
 OS HOMO SAPIENS (HUMAN).  
 OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;  
 OC EUTHERIA; PRIMATES.  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE; 97238921.  
 RA PAN G., O'ROURKE K., CHINNAIAN A.N., GENTZ R., EBNER R., NI J.,  
 RA DIXIT V.M.;  
 RL SCIENCE 276:111-113(1997).  
 DR EMBL; U90875; G1945072; -.  
 SQ SEQUENCE 468 AA; 50025 MW; 95AEP6SF CRC32;

Query Match 28.9%; Score 784; DB 2; Length 468;  
 Best Local Similarity 48.8%; Pred. No. 1.06e-128;  
 Matches 168; Conservative 60; Mismatches 79; Indels 37; Gaps 19;

Db 60 GQMGFAR-ARAGAGCPGPRARASPLRVHKTFFVY--VGVLLQV-VPSAAITK-L 113  
 Yq 5 GQSVPTASSARAGTGPARTASGTTPMLLDKILKLVVIVAVLLPVVDASATPQDEV 64

Db 114 HDOSITQWQESPL-GLCPGSHRSRPGACNCTBGGVGTNASNLPACLCTACKS 172  
 Yq 65 PQQVAPQO-QRSLAKEECPSGSRSETGCNCTBGGVGTNASNLPSCLLCTVCKS 123

Db 173 DEBERSPTTTRWACQCKPFTGNDNSAEMCKSCPGPMVKVADCTPWSIDCVHK 232  
 Yq 124 GQTKNSCTTTTDTVQCEKGSFQDKNSPDMCTRCCTGPGAGMKVSNCTPRSDIAKNE 183

Db 233 --ES-GN---GNH-INWIL-VVT-----LVPLLIVLVL-IVC-CC-----IG--SG- 267  
 Yq 184 SAASSTGKTAAEETVTTILGLASPYHYLIIVLVILAAVVGFSCKRKFISY 243

Db 268 C---GGDPKMRVCPNRLG-LLRGPGAEDNARNELISNADSLTFVSEQMEQSPADL 323  
 Yq 244 CSOGGGGPKVRHVLFRRCSPSRVPGAEDNARNETLSNRLQTPVSEQIQOE 307

Db 324 TGVTVSPGSAQCLLGPAAERQRRRLVPANEGDPT 367  
 Yq 304 TGVTVXPEEPQRLLEQAEAGCQRRRLVPVNDASD 342

Db 324 TGVTVXPEEPQRLLEQAEAGCQRRRLVPVNDASD 342

RESULT 9  
 ID 019131 PRELIMINARY; PRT; 471 AA.

AC 019131;  
 DT 01-JAN-1998 (TREMBLREL. 05, CREATED)  
 DT 01-JAN-1998 (TREMBLREL. 05, LAST SEQUENCE UPDATE)  
 DT 01-JAN-1998 (TREMBLREL. 05, LAST ANNOTATION UPDATE)  
 DE TUMOR NECROSIS FACTOR-RECEPTOR I.  
 GN TNF-RI.  
 OS BOS TAURUS (BOVINE).  
 OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;  
 OC EUTHERIA; ARTIODACTYLA.

RN [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=AORTA;  
 RA LEE E.-K., TALYOR M.J., KEHRLI M.E.;  
 RL SUBMITTED (AUG-1997) TO EMBL/GENBANK/DBJ DATA BANKS.  
 DR EMBL; U90937; G2290398; -.  
 DR PROSITE; PS00652; TNFR\_NGFR\_1; 3.  
 SQ SEQUENCE 471 AA; 51368 MW; 1D60FF4A CRC32;

Query Match 7.1%; Score 192; DB 4; Length 471;  
 Best Local Similarity 34.6%; Pred. No. 3.21e-14;  
 Matches 36; Conservative 16; Mismatches 41; Indels 11; Gaps 10;

Db 70 NDCP-GPGR-D-TD-CRVCAPT-YTALENHRLKRLCSRCRDENFQVEISPCVDDOTV 124  
 Yq 81 EEPAGSRSETGTGCNCTBGGVGTNASNLPSCLLCTVCKSG--QTKNSCTTTTDTV 138

Db 125 CGCRKNQFREYWGTFRCNLCSL-CPNGTVNIP-COERQDTIC 166

Yq 139 CQCEKSGSPD-KNSPEM-CRTCTCGCPGMVKNCTPRSDIK 180

RESULT 10  
 ID Q62327 PRELIMINARY; PRT; 459 AA.

AC Q62327;  
 DT 01-NOV-1996 (TREMBLREL. 01, CREATED)  
 DT 01-NOV-1996 (TREMBLREL. 01, LAST SEQUENCE UPDATE)  
 DT 01-JAN-1998 (TREMBLREL. 05, LAST ANNOTATION UPDATE)  
 DE TUMOR NECROSIS FACTOR RECEPTOR 2 MRNA (FRAGMENT).  
 OS MUS MUSCULUS (MOUSE).  
 OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;  
 OC EUTHERIA; RODENTIA.  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=MOD;  
 RX MEDLINE; 95178848.  
 RA POWELL E.E., WICKER L.S., PETERSON L.B., TODD J.A.;  
 RL MAMM. GENOME 5:726-727(1994).  
 DR EMBL; X76401; G433831; -.  
 DR PROSITE; PS00652; TNFR\_NGFR\_1; 2.  
 FT NOWRER 1 1  
 FT VARIANT 87 87 S -> T.  
 FT VARIANT 93 93 T -> I.  
 FT VARIANT 268 268 F -> I.  
 FT VARIANT 345 345 S -> F.  
 FT VARIANT 421 421 T -> C.  
 SQ SEQUENCE 459 AA; 48686 MW; 57791809 CRC32;

Query Match 7.0%; Score 191; DB 10; Length 459;  
 Best Local Similarity 27.6%; Pred. No. 4.71e-14;  
 Matches 29; Conservative 27; Mismatches 44; Indels 5; Gaps 5;

Db 61 CADCEASM-TYQWNNFRTLCSSSSSTDQVTRACTQKQVNCVACAGRYCALTKHS 119  
 Yq 96 CNCTBGGVGTNASNLPSCLLCTV-CSGQTKNSCTTTTDTVQCEKGSFQD-KNSPE 153

Db 120 SCRCQHLKSCGPGFVASSRPNMVKACACGTFSDTTSST 164

Yq 154 MCRTC-RTG-CPGGMVKNCTPRSDIKCNKESASSTGKTAAE 196

RESULT 11  
 ID Q85407 PRELIMINARY; PRT; 348 AA.

AC Q85407;  
 DT 01-NOV-1996 (TREMBLREL. 01, CREATED)  
 DT 01-NOV-1996 (TREMBLREL. 01, LAST SEQUENCE UPDATE)  
 DT 01-JAN-1998 (TREMBLREL. 05, LAST ANNOTATION UPDATE)  
 DE HOMOLOG OF VACCINIA VIRUS CDS 828R.  
 GN G2R.  
 OS VARIOLA VIRUS.  
 OC VIRIDAE; DS-DNA ENVELOPED VIRUSES; POXVIRIDAE; CHORDOPOXVIRINAE;

RESULT 15

ID Q14293 PRELIMINARY; PRT: 314 AA.

AC Q14293;  
DT 01-NOV-1996 (TRENBLREL. 01, CREATED)  
DT 01-NOV-1996 (TRENBLREL. 01, LAST SEQUENCE UPDATE)  
DT 01-JAN-1998 (TRENBLREL. 05, LAST ANNOTATION UPDATE)  
DE FAS SOLUBLE PROTEIN.  
OS HOMO SAPIENS (HUMAN).  
OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;  
OC EUETHERIA; PRIMATES.  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE; 95181785.  
RA CASCINO I., FIUCCI G., PAPOFF G., RUBERTI G.;  
RL J. IMMUNOL. 154:2706-2713(1995).  
DR EMBL; I47993; G695539; -.  
DR PROSITE; PS00652; TNFR\_NGFR\_1; 1.  
SQ SEQUENCE 314 AA; 35386 MW; F39D50D5 CRC32;

Query Match 6.7%; Score 182; DB 2; Length 314;  
Best Local Similarity 35.6%; Pred. No. 1.44e-12;  
Matches 32; Conservative 18; Mismatches 35; Indels 5; Gaps 4;

Db 82 CVPQBEKEYTDKAHSSKCRCKLCDBGHGLEVINCTRTQNTKCRCKPNFFCNSTVCE 141  
||| || :|| :: :| ||:| |: :|| :|| :|| :|  
Qy 96 CNPCTBEVDYTIASNNLPSCLLCTVCKSGQT-N-KSSCTTTRDTVCQCEKGSFQDKNSPE 153  
| | | | :|| :| :| :| :|| :|  
Db 142 HCDPC-TKCEGIIK--ECTLTSNTKCKEE 168  
| | | | :|| :| :| :| :|| :|  
Qy 154 MCRTRCTGCPRGNVKVSNTPTPSDIKCKNE 183

Search completed: Thu May 14 16:49:06 1998  
Job time : 52 secs.

## MORFON

Qy 154 MCRTCRTGCPRGMVKVSNCTPRSDIKCKNESAASSTGKTPAAEETV 199

RESULT 2  
 ID R11142 standard; Protein; 474 AA.  
 AC R11142;  
 DT 24-MAY-1991 (first entry)  
 DE TNF-R deduced from mTNF-R clone 11.  
 KW Tumour necrosis factor receptor; immune response; inflammation;  
 KW cachexia; septic shock.  
 OS Mus musculus strain C57BL/6.  
 FH Key Location/Qualifiers  
 FT peptide 1..22  
 FT /label= signal sequence  
 FT domain 234..265  
 FT /label= transmembrane region  
 PN EP-418014-A.  
 PD 20-MAR-1991.  
 PP 10-SEP-1990; 309875.  
 PR 11-SEP-1989; US-405370.  
 PR 13-OCT-1989; US-421417.  
 PR 10-MAY-1990; US-523635.  
 PA (IMMU) IMMUNEX CORP.  
 PI Smith CA, Goodwin RG, Beckmann PM;  
 DR WPI: 91-08220/12.  
 DR N-PSDB: Q10991.  
 FT New tumour necrosis factor -alpha and -beta receptors - and DNA  
 FT encoding these used to regulate immune responses in treatment of  
 FT cachexia, septic shock or side-effects of cytokine therapy.  
 FS Disclosure: Fig 3; 41pp; English.  
 CC The sequence was deduced from a clone isolated from library prepd.  
 CC from a murine T helper cell line, 7B3.  
 CC See also R11141.  
 SQ Sequence 474 AA;

Query Match 7.2%; Score 195; DB 2; Length 474;  
 Best Local Similarity 28.6%; Pred. No. 5.19e-07;  
 Matches 30; Conservative 27; Mismatches 43; Indels 5; Gaps 5;

Db 76 cdacdeam-ytgvrngfirtscsssscttdgveiractqknrvceagrycdlthg 134  
 | | : : | | : : | | : : | | : : | | : : | | : : | | : :  
 Qy 96 CNPCTBGVDITIASNLPSCLLCTV-CXSGQYKNSCTTTRDTVQCXGSGFDQ-KNSPE 153  
 Db 135 scrgcmrlskcpgpgfvassrapngnwlckacpgtfdtstsd 179  
 | | | : | | | : | | : : | | : : | | : : | | : :  
 Qy 154 MCRITC-RTPGPMWVSNCTPRSDIKCKNESASSTGTPAAE 196

RESULT 3  
 ID R28084 standard; Protein; 335 AA.  
 AC R28084;  
 DT 12-MAR-1993 (first entry)  
 DE Human cell surface antigen.  
 KW Fas antigen; apoptosis; p58; NGFR/TNFR family.  
 OS Homo sapiens.  
 FH Key Location/Qualifiers  
 FT peptide 1..16  
 FT /label= signal  
 FT protein 17..335  
 FT /label= Fas\_antigen  
 FT modified\_site 118..120  
 FT /label= N-glycosylation\_site  
 FT /note= "putative"  
 FT modified\_site 136..138  
 FT /label= N-glycosylation\_site  
 FT /note= "putative"  
 FT domain 174..190  
 FT /label= transmembrane  
 FT domain 17..173  
 FT /label= extracellular  
 FT /note= "cysteine-rich"  
 FT domain 191..335  
 FT /label= cytoplasmic  
 PN EP-510691-A.  
 PD 28-OCT-1992.

PF 24-APR-1992; 107060.  
 PR 26-APR-1991; JP-125234.  
 PA (OSAB-) OSABA BIOSCIENCE INST.  
 PI Itoh N, Nagata S, Yonehara S;  
 DR WPI: 92-358914/44.  
 DR N-PSDB: Q29959.  
 PT DNA encoding human cell surface antigen - used to clarify  
 PT apoptosis mechanism of various types of cell, and to prepare  
 PT monoclonal antibodies that react with tumour cells expressing Fas  
 PS Claim 3; Fig 1 and 2; 27pp; English.  
 CC The Fas antigen is implicated in apoptosis. A cDNA clone encoding  
 CC the antigen was isolated (pF58) and the amino acid sequence of Fas  
 CC was deduced from it. The mature protein has a calculated mol.wt. of  
 CC 36,000 and is a member of the NGFR/TNFR family of cell-surface  
 CC membrane proteins. The inventors claim a protein comprising at  
 CC least the extracellular domain of Fas antigen.  
 SQ Sequence 335 AA;

Query Match 7.0%; Score 191; DB 5; Length 335;  
 Best Local Similarity 35.1%; Pred. No. 1.11e-06;  
 Matches 34; Conservative 21; Mismatches 37; Indels 5; Gaps 4;

Db 82 cvpcgeqekytdkafhskrrrrcldeghgleveinctrtgntkckrckpffnctvce 141  
 | | | | : | : : | | : : | : : : | : | : | : | : | : | :  
 Qy 96 CNPCTBGVDITIASNLPSCLLCTVCKSGQT-N-KSSCTTTRDTVQCXGSGFDQ-KNSPE 153  
 Db 142 hdcpc-tkceghlik-ecitltsntkckegsrnlg 175  
 | | | : | : | : | : | : | : | : | : | : | : | : | :  
 Qy 154 MCRITC-RTPGPMWVSNCTPRSDIKCKNESASSTG 190

RESULT 4  
 ID R78606 standard; Protein; 335 AA.  
 AC R78606;  
 DT 15-FEB-1996 (first entry)  
 DE Human Fas protein.  
 KW Plasmid pF58; human Fas cDNA; soluble membrane protein;  
 KW antibody production; diseases; treatment; prevention.  
 OS Homo sapiens.  
 FH Key Location/Qualifiers  
 FT peptide 1..16  
 FT /label= sig\_peptide  
 FT peptide 17..335  
 FT /label= mat\_peptide  
 PN J07115988-A.  
 PD 09-MAY-1995.  
 PF 26-OCT-1993; 267644.  
 PR 26-OCT-1993; JP-267644.  
 PA (NIBS ) JAPAN TOBACCO INC.  
 DR WPI: 95-202847/27.  
 DR N-PSDB: Q95297.

PT Preparation of soluble membrane proteins - for their use in antibody  
 PT production for the treatment and prevention of related diseases  
 PS Example 1; Pages 15-17; 5pp; Japanese.  
 CC R78606 (human Fas protein) is encoded by the plasmid pF58 which  
 CC contains hFas cDNA. The plasmid was used in the construction of an  
 CC expression vector for the prodn. of recombinant soluble membrane  
 CC proteins. The proteins can be used in antibody prodn. for the  
 CC treatment and prevention of related diseases.  
 SQ Sequence 335 AA;

Query Match 7.0%; Score 191; DB 14; Length 335;  
 Best Local Similarity 35.1%; Pred. No. 1.11e-06;  
 Matches 34; Conservative 21; Mismatches 37; Indels 5; Gaps 4;

Db 82 cvpcgeqekytdkafhskrrrrcldeghgleveinctrtgntkckrckpffnctvce 141  
 | | | | : | : : | | : : | : : : | : | : | : | : | : | :  
 Qy 96 CNPCTBGVDITIASNLPSCLLCTVCKSGQT-N-KSSCTTTRDTVQCXGSGFDQ-KNSPE 153  
 Db 142 hdcpc-tkceghlik-ecitltsntkckegsrnlg 175  
 | | | : | : | : | : | : | : | : | : | : | : | : | :  
 Qy 154 MCRITC-RTPGPMWVSNCTPRSDIKCKNESASSTG 190

Db 58 kntntgtctpcasdt-ftsrnnhlpaclscngcdsngvetrsentthnricdcapgyyc 116  
:: |||: :| :||:| | | | : || |: :| | :  
Qy 89 RSEYTGACNPCTEGVDYTIASNNPLSCLLCTV-CKSGQTNKSSCTTTEDTVQCCEKGSFQ 147



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RESULT 11
ID R99682 standard; Protein; 314 AA.
AC R99682;
DT 10-OCT-1996 (first entry)
DE Human Fas soluble antigen Fas dell.
KW Fas antigen; autoimmune disease; systemic lupus erythematosus; SLE;
KW angliomunoblastic lymphadenopathy; AILD.
OS Homo sapiens.
FH Key Location/Qualifiers
FT peptide 1..16
FT /label= Sig_peptide
FT protein 17..314
FT /label= Mat_protein
FT /note= "soluble Fas dell antigen"
FT domain 17..169
FT /label= Extracellular_domain
FT /note= "the 5 C-terminal residues of the
FT Fas antigen extracellular domain are
FT deleted in Fas dell"
FT domain 169..314
FT /label= Cytoplasmic_domain
FT peptide 164..173
FT /note= "preferred peptide from breakpoint region
FT (claim 4, page 132)"
FT peptide 164..174
FT /note= "preferred peptide from breakpoint region"
FT peptide 161..171
FT /note= "preferred peptide from breakpoint region"
PW W09620206-A1.
PD 04-JUL-1996.
PF 22-DEC-1995; U17083.
PR 23-DEC-1994; US-371263.
PA (UABR) UAB RES FOUNDED.
PI Cheng J, Liu C, Mount J, Zhou T;
DR WPI: 96-321796/32.
DR N-PSDB: T34527.
PT Natural, soluble form of Fas antigen secreted by human cells is
PT result of alternative mRNA processing - used to diagnose
PT Fas-associated disease, e.g. systemic lupus erythematosus
PS Claim 4; Page 114-16; 152pp; English.
CC A natural, soluble Fas antigen variant (R99682), designated Fas
CC dell, and other Fas variants (R99683-85) are derived by alternative
CC splicing of Fas gene transcripts. A cDNA clone (T34527) coding for
CC the variant was obt'd. from human peripheral blood mononuclear cells.
CC The Fas dell variant lacks the transmembrane domain of insoluble
CC Fas antigen (R99681). Recombinant dell variant, or fragments of
CC it, can be expressed in prokaryotic or eukaryotic (e.g. COS) cells.
CC Detection of increased levels of soluble forms of Fas antigen can
CC be used to diagnose autoimmune diseases, esp. systemic lupus
CC erythematosus and angliomunoblastic lymphadenopathy.
SQ Sequence 314 AA;

Query Match 6.7%; Score 182; DB 18; Length 314;
Best Local Similarity 35.6%; Pred. No. 6.12e-06;
Matches 32; Conservative 18; Mismatches 35; Indels 5; Gaps 4;

Db 82 cypcgeqktydkahfsskrrrrcddegheveinctrtgtkrckrcpffcnstnce 141
| | | | | : | : | : | : | : | : | : | : |
Qy 96 CNPCTGCVDTTASNNPLSCCLTCVCKSGQT-N-KSSCTTTRDTVQCEKSGFDKNSPE 153

Db 142 hdcpc-tkceghlik-ecitltsntckee 168
| | | | | : | | : | | | |
Qy 154 MCRTRCTGCGPGMWVSNCTPRSDIKCKNE 183

RESULT 12
ID R76238 standard; Protein; 314 AA.
AC R76238;
DT 06-NOV-1995 (first entry)
DE Fas-delta-TM.
KW Fas-delta-TM; transmembrane deletion; apoptosis; antibody;
KW adoptive immunotherapy; transgenic animal.
OS Homo sapiens.

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FH Key Location/Qualifiers
FT peptide 1..16
FT /label= Sig_peptide
PW W09511701-A.
PD 26-MAY-1995.
PF 15-NOV-1994; U13173.
PR 15-NOV-1993; US-152443.
PA (LMBR) LMBR BIOTECHNOLOGY INC.
PI Barr PJ, Kiefer MC, Shapiro JP;
DR WPI: 95-200120/26.
DR N-PSDB: Q89379.
PT New nucleic acid encoding Fas protein without its trans-membrane region
PT and related vectors, transformed cells, transgenic animals, protein and
PT antibodies, useful for control of Fas mediated apoptosis
PS Claim 3; Fig.3-1 to 3-4; 38pp; English.
CC mRNA was obt'd. from human lymphocytes and PCR was used to make
CC cDNA specific for Fas-delta-TM (i.e. Fas lacking the transmembrane
CC region) mRNA. The PCR product was ligated into pBluescript and the
CC recombinant plasmid was used to transfect E. coli DH5-alpha cells. The
CC insert sequence of pBluescript-Fas-delta-TM encoded the protein
CC given in R76238.
SQ Sequence 314 AA;

Query Match 6.7%; Score 182; DB 13; Length 314;
Best Local Similarity 35.6%; Pred. No. 6.12e-06;
Matches 32; Conservative 18; Mismatches 35; Indels 5; Gaps 4;

Db 82 cypcgeqktydkahfsskrrrrcddegheveinctrtgtkrckrcpffcnstnce 141
| | | | | : | : | : | : | : | : | : | : |
Qy 96 CNPCTGCVDTTASNNPLSCCLTCVCKSGQT-N-KSSCTTTRDTVQCEKSGFDKNSPE 153

Db 142 hdcpc-tkceghlik-ecitltsntckee 168
| | | | | : | | : | | | |
Qy 154 MCRTRCTGCGPGMWVSNCTPRSDIKCKNE 183

RESULT 13
ID R24083 standard; Protein; 159 AA.
AC R24083;
DT 05-NOV-1992 (first entry)
DE Truncated TNF-alpha 55kd receptor.
KW tumour necrosis factor alpha; extracellular binding domain;
KW treatment; pulmonary diseases; septic shock; HIV infection; AIDS;
KW malaria; viral meningitis; graft versus host disease;
KW autoimmune disease; rheumatoid arthritis.
OS Homo sapiens.
PW W09207076-A.
PD 30-APR-1992.
PF 18-OCT-1991; G01826.
PR 18-OCT-1990; GB-022648.
PA (CHAR) CHARING CROSS SUNLEY RES CENT.
PI Brennan FM, Feldmann M, Gray PW, Turner MJC;
DR WPI: 92-167156/20.
DR N-PSDB: Q24444.
PT New polypeptide capable of binding human TNF alpha - comprises
PT first three cysteine-rich subdomains of TNF alpha receptor for
PT treating autoimmune disease, septic shock, HIV etc.
PS Example 1; Fig 10; 43pp; English.
CC This sequence is a truncated TNF-alpha receptor derivative
CC as encoded in pdeltaIII. This was produced as described in
CC Q24444. This derivative lacks the third cysteine rich subdomain.
CC It could be used to regulate TNF-alpha mediated responses by binding
CC and sequestering human TNF-alpha e.g. in the treatment of pulmonary
CC diseases, septic shock, HIV infection, malaria, viral meningitis,
CC graft versus host disease and autoimmune diseases, esp. rheumatoid
CC arthritis.
CC See also Q24440-51, R24000, R24080-84, R27585, Q29236-8
SQ Sequence 159 AA;

Query Match 6.6%; Score 179; DB 4; Length 159;
Best Local Similarity 41.2%; Pred. No. 1.08e-05;
Matches 28; Conservative 7; Mismatches 30; Indels 3; Gaps 3;

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RESULT 15
ID R85072 standard; Protein: 326 AA.
AC R85072;
DT 16-APR-1996 (first entry)
DE Myxoma virus T2 protein.
KW Myxoma virus; immunosuppressive; cytokine antagonist;
KW tumour necrosis factor antagonist; therapeutic; cachexia;
KW septic shock.
OS Myxoma virus.
PN US5464938-A.
PD 07-NOV-1995.
PF 18-ADG-1994; 292549.
PR 19-OCT-1992; US-963330.
PA (TMV ) Immunex Corp.
PI Goodwin RG, Smith CA
DR WPI, 95-40386/51.
DR N-PSDB: T02471.
PT New soluble viral proteins that bind tumour necrosis factor - for
PT treating cachexia, septic shock, side effects of TNF therapy etc.,
PT also useful in assays, affinity purification. And antibody prodn.
PS Claim 1; Columns 31-32; 21pp; English.
CC The myxoma virus T2 protein is a soluble viral protein which
CC binds tumour necrosis factor (TNF), thus inhibiting TNF binding

```

\*\*\*\*\*  
 M A S A R C H (TM)  
 \*\*\*\*\*

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MPSrch\_pp protein - protein database search, using Smith-Waterman algorithm

Run on: Thu May 14 16:49:23 1998; MasPar time 16.85 Seconds  
 836.713 Million cell updates/sec  
 Tabular output not generated.

Title: >US-08-918-874-1  
 Description: (1-386) from US08918874.pep  
 Perfect Score: 2715  
 Sequence: 1 MGLWGQSVPTASARAGNYP.....VGSEKLFYEEDAGSATSCL 386

Scoring table: PAM 150  
 Gap 11

Searched: 120446 seqs, 36531193 residues

Post-processing: Minimum Match 0%  
 Listing first 45 summaries

Database: pir56  
 1:pir1 2:pir2 3:pir3 4:pir4 5:nrlr3d

Statistics: Mean 46.756; Variance 102.161; scale 0.458

Pred. No. is the number of results predicted by chance to have a  
 score greater than or equal to the score of the result being printed,  
 and is derived by analysis of the total score distribution.

#### SUMMARIES

Result	Query	No.	Score	Match	Length	DB	ID	Description	Pred. No.
1	191	7.0	335	2	A40036	apoptosis-mediating s	8.42e-13		
2	191	7.0	459	2	I48854	gene murine tumour ne	8.42e-13		
3	189	7.0	474	2	B38634	tumor necrosis factor	1.70e-12		
4	187	6.9	349	2	D36858	gene G4R protein - va	3.43e-12		
5	185	6.8	427	1	GQHUN	nerve growth factor r	6.91e-12		
6	184	6.8	461	2	JC4302	tumor necrosis factor	9.79e-12		
7	182	6.7	314	2	I37383	PAS soluble protein -	1.96e-11		
8	180	6.6	326	1	GQVZML	T2 protein - myxoma v	3.93e-11		
9	176	6.5	324	2	JC2395	Fas antigen - rat	1.56e-10		
10	177	6.5	327	2	A46484	apoptosis-mediating m	1.11e-10		
11	173	6.4	139	5	1TNR8	tumor necrosis factor	4.36e-10		
12	173	6.4	140	5	1NCPA	tumor necrosis factor	4.36e-10		
13	173	6.4	142	5	1NCFB	tumor necrosis factor	4.36e-10		
14	173	6.4	158	5	1EXTB	tumor necrosis factor	4.36e-10		
15	173	6.4	160	5	1EXTA	tumor necrosis factor	4.36e-10		
16	173	6.4	455	1	GQHU11	tumor necrosis factor	4.36e-10		
17	170	6.3	416	2	JN0006	nerve growth factor r	1.21e-09		
18	171	6.3	425	2	A26431	nerve growth factor r	8.63e-10		
19	166	6.1	325	2	B43592	T2 protein - rabbit f	4.69e-09		
20	159	5.9	461	1	GQRT71	tumor necrosis factor	4.87e-08		
21	158	5.8	461	2	A35356	tumor necrosis factor	6.79e-08		
22	156	5.7	454	1	GQNS71	tumor necrosis factor	1.31e-07		
23	156	5.7	454	2	I57826	tumor necrosis factor	1.31e-07		

24	151	5.6	271	2	S12783	OX40 antigen precursor	6.75e-07
25	151	5.6	272	2	I48700	gene ox40 protein - m	6.75e-07
26	144	5.3	256	2	B32393	T-cell antigen 4-1BB	6.43e-06
27	144	5.3	435	2	I54182	tumor necrosis factor	6.43e-06
28	137	5.0	255	2	JT0752	lymphocyte activation	5.86e-05
29	134	4.9	260	1	A46517	CD27 antigen precursor	1.49e-04
30	127	4.7	493	2	JC5486	membrane glycoprotein	1.26e-03
31	125	4.6	595	2	A42086	CD30 antigen precursor	2.29e-03
32	118	4.3	250	1	A49053	CD27 antigen precursor	1.80e-02
33	111	4.1	183	2	S52904	virion protein j13L -	1.32e-01
34	111	4.1	185	2	S52903	virion protein j13L -	1.32e-01
35	110	4.1	277	2	A60771	B-cell activation pro	1.74e-01
36	110	4.1	512	2	I80311	sepC protein - Escher	1.74e-01
37	108	4.0	85	2	I55492	myosin heavy chain -	3.02e-01
38	109	4.0	176	2	S52914	virion protein j13L -	2.29e-01
39	109	4.0	189	2	S52907	virion protein j13L -	2.29e-01
40	109	4.0	191	2	S52905	virion protein j13L -	2.29e-01
41	109	4.0	420	2	B38104	LFY floral meristem i	2.29e-01
42	109	4.0	1790	1	MNFEB1	laminin chain B1 prec	2.29e-01
43	108	4.0	3133	2	S52093	hemocytin - silkworm	3.02e-01
44	105	3.9	189	2	S52902	virion protein j13L -	6.84e-01
45	104	3.8	431	1	BWSS5Y	preprotein translocas	8.95e-01

#### ALIGNMENTS

RESULT 1  
 ENTRY A40036 #type complete

TITLE apoptosis-mediating surface antigen Fas precursor - humanALTERNATE\_N  
 ORGANISM #formal\_name Homo sapiens #common\_name man  
 DATE 17-Jan-1992 #sequence\_revision 17-Jan-1992 #text\_change 10-Sep-1997

ACCESSIONS A40036; S24543; A38142  
 REFERENCE A40036

#authors Itoh, N.; Yonehara, S.; Ishii, A.; Yonehara, M.; Mizushima, S.I.; Sameshima, M.; Hase, A.; Seto, Y.; Nagata, S.  
 #journal Cell (1991) 66:233-243  
 #title The polypeptide encoded by the cDNA for human cell surface antigen Fas can mediate apoptosis.  
 #cross-references MIMD:91309137  
 #accession A40036  
 #status preliminary  
 #molecule\_type mRNA  
 #residues 1-335 #label ITO  
 #cross-references GB:M67454; NID:g182409; PID:g182410

REFERENCE S24543  
 #authors Krammer, P.H.  
 #submission submitted to the EMBL Data Library, February 1992  
 #accession S24543

#status preliminary  
 #molecule\_type mRNA  
 #residues 1-335 #label KRA  
 #cross-references EMBL:X63717; NID:g28741; PID:g28742

REFERENCE A38142  
 #authors Oehm, A.; Behrmann, I.; Falk, W.; Pawlita, M.; Maier, G.; Klas, C.; Li-Weber, M.; Richards, S.; Dhein, J.; Trauth, B.C.; Pousting, R.; Krammer, P.H.  
 #journal J. Biol. Chem. (1992) 267:10709-10715  
 #title Purification and molecular cloning of the APO-1 cell surface antigen, a member of the tumor necrosis factor/nerve growth factor receptor superfamily. Sequence identity with the Fas antigen.  
 #cross-references MIMD:92268122  
 #accession A38142

#status preliminary; not compared with conceptual translation  
 #molecule\_type nucleic acid  
 #residues 1-134, '0', 136-335 #label OEH  
 #experimental\_source SW6.4 cells  
 #note sequence extracted from NCBI backbone (NCBIPI:103810)  
 #note in NCBI backbone the source is designated as mouse

GENETICS  
 #gene GDB:AP1

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cross-references MIMD:91187885
#accession B38634
#molecule_type mRNA
#residues 1-474 ##label LEW
#cross-references GB:M60469; NID:g199827; PID:g199828
REFERENCE
A40254
#authors Goodwin, R.G.; Anderson, D.; Jerzy, R.; Davis, T.; Brannan,
C.I.; Copeland, N.G.; Jenkins, N.A.; Smith, C.A.
#journal Mol. Cell. Biol. (1991) 11:3020-3026
#title Molecular cloning and expression of the type 1 and type 2
murine receptors for tumor necrosis factor.
#cross-references MIMD:91246168
#accession A40254
#molecule_type mRNA
#residues 1-474 ##label GOO
#cross-references GB:M60469; NID:g199827; PID:g199828
REFERENCE
S54816
#authors Tsomerngrhls, M.; Fellowes, R.; Feldmann, M.; Chernaiovsky,
Y
#submission submitted to the EMBL Data Library, May 1995
#description Characterization of the promoter region of the murine p75-TNF
receptor.
#accession S54816
#status preliminary
#molecule_type DNA
#residues 1-22 ##label KIS
#cross-references EMBL:X87128; NID:g809043; PID:g809044
CLASSIFICATION
#superfamily tumor necrosis factor receptor type 2; NGF
receptor repeat homology
KEYWORDS
cytokine receptor; transmembrane protein
FEATURE
1-22 #domain signal sequence #status predicted #label SIG\
23-474 #product tumor necrosis factor receptor type 2 #status
predicted #label MAT\
40-77 #domain NGF receptor repeat homology #label NG1\
79-120 #domain NGF receptor repeat homology #label NG2\
166-203 #domain NGF receptor repeat homology #label NG4
SUMMARY
#length 474 #molecular-weight 50319 #checksum 7767
Query Match 7.0% Score 189; DB 2; Length 474;
Best Local Similarity 27.6%; Pred. No. 1.70e-12;
Matches 29; Conservative 27; Mismatches 44; Indels 5; Gaps 5;
Db 76 CACCAAM-TTQWQNFRTCLSCSSCTTDQVEIRACTQQRNVCAEAGRYCALYTHSG 134
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Qy 96 CNCPCTGVDYTIASNLNCSLLCYT-CXSGSQNKSCCTTRDQVQCCGSPFD-KNSPE 153
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 135 SCRCQMRSLKCGPGVGVAASSRPNGLVCKACAPGTFSDTTSSTD 179
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Qy 154 MCRTC-RTG-CPRMGVKYSNCTPRSDIKCNKNSAASGTGTFAAE 196
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
RESULT 4
ENTRY D36858 #type complete
TITLE gene G4R protein - variola virusALTERNATE_NAMES B28R protein (COP)
ORGANISM #formal_name variola virus
DATE 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change
10-Sep-1997
ACCESSIONS D36858; D36888; S32385; S35987
REFERENCE A36859
#authors Blinov, V.M.
#submission submitted to GenBank, November 1992
#description not shown.
#accession D36858
#status preliminary
#molecule_type DNA
#residues 1-349 ##label BLI
#cross-references GB:X69198; NID:g456758; PID:g457087
#experimental_source strain India:1967, ssp. major, isolate Ind3
REFERENCE S46868
#authors Kolykhalov, A.A.; Blinov, V.M.; Gytarov, V.V.; Pozdnayakov,
S.G.; Chizhikov, V.E.; Frolov, I.V.; Totmenin, A.V.;

```

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proof to follow the nucleotide translation from a published report
```

REFERENCE S21689  
#authors Vissavajjhala, P.; Leszyk, J.D.; Lin-Goerke, J.; Ross, A.H.  
#journal Ann. Biochem. Biophys. (1992) 294:244-252  
#title Structural domains of the extracellular domain of human nerve growth factor receptor detected by partial proteolysis.

#cross-references MUID:92I98017  
#accession S21689  
#status preliminary  
#molecule\_type protein  
#residues 183-208 #label VIS

REFERENCE I57638  
#authors Sehgal, A.; Patil, N.; Chao, M.  
#journal Mol. Cell. Biol. (1988) 8:3160-3167  
#title A constitutive promoter directs expression of the nerve growth factor receptor gene.

#cross-references MUID:89096903  
#accession I57638  
#status preliminary; translated from GB/EMBL/DDBJ  
#molecule\_type DNA  
#residues 1-22 #label RES  
#cross-references GB:M21621; NID:G189206; PID:G189207

COMMENT This receptor is found on sensory and sympathetic neurons; on neuroblastoma cells, and on a variety of nonneuronal derivatives of the neural crest.

COMMENT The cysteine-rich region of the extracellular domain may form part or all of the NGF-binding site.

COMMENT This protein is thought to form a high-affinity receptor when it associates with the 140K trk proto-oncogene, which contains an intracellular tyrosine kinase domain.

COMMENT This receptor undergoes both N- and O-linked glycosylation.

GENETICS  
#gene GDB:NGFR  
#cross-references GDB:I20234; OMIM:162010  
#map\_position 17q21-17q22

CLASSIFICATION #superfamily nerve growth factor receptor; NGF receptor repeat homology

KEYWORDS duplication; glycoprotein; heterodimer; monomer; phosphoprotein; receptor; transmembrane protein

FEATURE  
1-28 #domain signal sequence \$status predicted \$label SIG\  
29-427 #product nerve growth factor receptor \$status experimental \$label MAT\  
29-250 #domain extracellular \$status predicted \$label EXT\  
29-190 #region cysteine-rich\  
32-65 #domain NGF receptor repeat homology \$label NG1\  
67-108 #domain NGF receptor repeat homology \$label NG2\  
109-147 #domain NGF receptor repeat homology \$label NG3\  
149-189 #domain NGF receptor repeat homology \$label NG4\  
197-248 #region serine/threonine-rich\  
251-272 #domain transmembrane \$status predicted \$label TRM\  
273-427 #domain intracellular \$status predicted \$label INT\  
60 #binding-site carboxyethate (Asn) (covalent) \$status predicted

SUMMARY #length 427 #molecular-weight 45183 #checksums 7426

Query Match 6.8%; Score 185; DB 1; Length 427;  
Best Local Similarity 29.4%; Pred. No. 6.91e-12;  
Matches 25; Conservative 21; Mismatches 37; Indels 2; Gaps 2;

Dd 123 CECPLDSVTFSDVSVAETPCPKCTEVCGLGSMSAPCEAADDVCRCAQYGYQD-ETTGRS 122  
|::||::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|  
Qy 96 NCNPTGSDVTITASNWLLPSCILCTIVCKSGQTNNSSCSTTRDTVCQCEKSGFDQNNSPEMC 155

Dd 123 EACRV-CRAGSLGVFSQCDKNQTVIC 146  
:|| || | || |::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|  
Qy 156 RICTRTCGPRGMVSVSNCTPRDIKC 180

RESULT 6  
ENTRY JC4302 #type complete

Query Match 6.7%; Score 182; DB 2; Length 314;  
Best Local Similarity 35.6%; Pred. No. 1.96e-11;  
Matches 32; Conservative 18; Mismatches 35; Indels 5; Gaps 4;

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#accession JC2195
#molecule_type mRNA
#residues 1-324 ##label KIM
#cross-references DDBJ:D26112; NID:q468486; PDB:1d005650; PDB:q468487
#experimental source thymus

#accession PC2246
#molecule_type mRNA
#residues 1-62,'RFT' ##label KI2
#cross-references DDBJ:D26113; NID:q468488; PDB:1d005651; PDB:q468489
#experimental source liver
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REFERENCE	A66195
#authors	Nalmsmith, J.H.; Sprang, S.R.
#submission	submitted to the Brookhaven Protein Data Bank, October 1994

TITLE tumor necrosis factor receptor extracellular domain, chain B  
 PDB\_TITLE extracellular domain of the 55kDa tumor necrosis factor  
 ORGANISM receptor, crystallized at ph3.7 in p 21 21 21.  
 #name Homo sapiens #common\_name man  
 #note expressed in Escherichia coli, the construct contains  
 residues 12 to 172 of the mature sequence of the entire  
 receptor, residue 11 is mutated to met as a result of the  
 expression system  
 REFERENCE A65560  
 #authors Naismith, J.H.; Sprang, S.R.  
 #submission submitted to the Brookhaven Protein Data Bank, July 1996  
 #cross-references PDB:1XTX  
 REFERENCE TM026251  
 #authors Naismith, J.H.; Devine, T.Q.; Brandhuber, B.J.; Sprang, S.R.  
 #journal J. Biol. Chem. (1995) 270:13303  
 #title Crystallographic evidence for dimerization of unliganded  
 tumor necrosis factor receptor.  
 REFERENCE TM026252  
 #authors Rodseth, L.E.; Brandhuber, B.J.; Devine, T.Q.; Eck, M.J.; Hale, K.; Naismith, J.H.; Sprang, S.R.  
 #journal J. Mol. Biol. (1994) 239:332  
 #title Two crystal forms of the extracellular domain of type I tumor  
 necrosis factor receptor.  
 REFERENCE A40737  
 #authors Banner, D.W.; D'Arcy, A.; Janes, W.; Czystal, R.; Schoenfeld, H.J.; Broger, C.; Loetscher, H.; Lesslauer, W.  
 #journal Cell (1993) 73:431-445  
 #title Crystal structure of the soluble human 55 kd TNF  
 receptor-human TNFbeta complex: implications for TNF  
 receptor activation.  
 COMMENT Resolution: 1.85 angstroms  
 COMMENT Determination: X-ray diffraction  
 COMMENT R-value: no refinement  
 KEYWORDS binding protein; cytokine; signalling protein  
 FEATURE  
 68-70 #region helix (right hand 3-10)\  
 143-145 #region helix (right hand 3-10)\  
 9-11,19-21 #region beta sheet\  
 133-136,139-142 #region beta sheet\  
 27-31,41-44 #region beta sheet\  
 73-76,85-87 #region beta sheet\  
 92-98,101-106 #region beta sheet\

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113-117,126-129  #region beta sheet\
5-19             #disulfide_bonds\
20-33            #disulfide_bonds\
23-42            #disulfide_bonds\
45-60            #disulfide_bonds\
63-78            #disulfide_bonds\
66-86            #disulfide_bonds\
88-104           #disulfide_bonds\
107-119          #disulfide_bonds\
110-127          #disulfide_bonds\
129-140          #disulfide_bonds\
143-156          #disulfide_bonds\
146-152          #disulfide_bonds\
SUMMARY          #length 158 #molecular-weight 17827 #checksum 5022

Query Match      6.4%; Score 173; DB 5; Length 158;
Best Local Similarity 37.1%; Pred. No. 4.36e-10;
Matches 33; Conservative 12; Mismatches 37; Indels 7; Gaps 6;

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Db 42 CREDSG-SFTASSENHLRLCLSCSKCKEMQVEISSCTVDRDTVCQCKNKQYHTWSEN 100
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Qy 96 CNMCTBGVDYTIASNNLPSCLLCTVC-KS-GQTNKSSCTTTRDTVCQCEKGSFDQKNPSE 153

Db 101 LFQCFNCSL-CLMGTVHLS-CQEKQNTVC 127
   : | | | | | | | | | : | : |
Qy 154 M--CRITCRGCGPRGMKVSNCCTPRSDIKC 180

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```

RESULT 15
ENTRY      LEXTA      #type complete

TITLE      tumor necrosis factor receptor extracellular domain, chain A
PDB_TITLE  extracellular domain of the 55kda tumor necrosis factor
            receptor. crystallized at ph3.7 in p 2l 2l 2l.
ORGANISM   #formal_name Homo sapiens #common_name man
            #note expressed in Escherichia coli, the construct contains
            residues 12 to 172 of the mature sequence of the entire
            receptor. residue 11 is mutated to met as a result of the
            expression system
REFERENCE  A65560
            #authors Naismith, J.H.; Sprang, S.R.
            #submission submitted to the Brookhaven Protein Data Bank, July 1996
            #cross-references PDB:LEX
REFERENCE  TN026248
            #authors Naismith, J.H.; Devine, T.Q.; Brandhuber, B.J.; Sprang, S.R.
            #journal J. Biol. Chem. (1995) 270:13303
            #title Crystallographic evidence for dimerization of unliganded
            tumor necrosis factor receptor.
REFERENCE  TN026249
            #authors Rodseth, L.E.; Brandhuber, B.; Devine, T.Q.; Eck, M.J.; Hale,
            X.; Naismith, J.H.; Sprang, S.R.
            #journal J. Mol. Biol. (1994) 239:332
            #title Two crystal forms of the extracellular domain of type i tumor
            necrosis factor receptor.
REFERENCE  A40737
            #authors Banner, D.W.; D'Arcy, A.; Janes, W.; Gentz, R.; Schoenfeld,
            H.J.; Broger, C.; Loetscher, H.; Lesslauer, W.
            #journal Cell (1993) 73:431-445
            #title Crystal structure of the soluble human 55 kd TNF
            receptor-human TNFbeta complex: implications for TNF
            receptor activation.
COMMENT    Resolution: 1.85 angstroms
COMMENT    Determination: X-ray diffraction
COMMENT    R-value: no refinement
KEYWORDS   binding protein; cytokine; signalling protein
FEATURE
66-68      #region helix (right hand 3-10)\
141-143    #region helix (right hand 3-10)\
151-154    #region helix (right hand alpha)\
7-9,17-19  #region beta sheet\
131-134,137-140 #region beta sheet\
25-29,39-42 #region beta sheet\
71-74,83-85 #region beta sheet\

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```

90-96,99-104 #region beta sheet\
111-115,124-127 #region beta sheet\
3-17          #disulfide_bonds\
18-31         #disulfide_bonds\
21-40         #disulfide_bonds\
43-58         #disulfide_bonds\
61-76         #disulfide_bonds\
64-84         #disulfide_bonds\
86-102        #disulfide_bonds\
105-117       #disulfide_bonds\
108-125       #disulfide_bonds\
127-138       #disulfide_bonds\
141-154       #disulfide_bonds\
144-150       #disulfide_bonds\
SUMMARY       #length 160 #molecular-weight 18065 #checksum 2297

Query Match      6.4%; Score 173; DB 5; Length 160;
Best Local Similarity 37.1%; Pred. No. 4.36e-10;
Matches 33; Conservative 12; Mismatches 37; Indels 7; Gaps 6;

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Db 40 CRECSG-SFTASSENHLRLCLSCSKCKEMQVEISSCTVDRDTVCQCKNKQYHTWSEN 98
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Qy 96 CNMCTBGVDYTIASNNLPSCLLCTVC-KS-GQTNKSSCTTTRDTVCQCEKGSFDQKNPSE 153

Db 99 LFQCFNCSL-CLMGTVHLS-CQEKQNTVC 125
   : | | | | | | | | | : | : |
Qy 154 M--CRITCRGCGPRGMKVSNCCTPRSDIKC 180

```

Search completed: Thu May 14 16:49:54 1998  
Job time : 31 secs.



\*\*\*\*\*  
 MPSRCH  
 (TM)  
 \*\*\*\*\*

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MPSrch\_gp protein - protein database search, using Smith-Waterman algorithm

Run on: Thu May 14 16:47:33 1998; MasPar time 11.24 Seconds  
 861.719 Million cell updates/sec  
 Tabular output not generated.

Title: >US-08-918-874-1  
 Description: (1-386) from US08918874.pep  
 Perfect Score: 2715  
 Sequence: 1 MGLMGQSVPTASSARAGRP.....VGSEKLFYEDEAGSATSC 386

Scoring table: PAM 150  
 Gap 11

Searched: 69112 seqs, 25083644 residues

Post-processing: Minimum Match 0%  
 Listing first 45 summaries

Database: swiss-prot35  
 l:swiss1

Statistics: Mean 48.960; Variance 85.763; scale 0.571

Pred. No. is the number of results predicted by chance to have a  
 score greater than or equal to the score of the result being printed,  
 and is derived by analysis of the total score distribution.

#### SUMMARIES

Result	Query	No.	Score	Match	Length	ID	Description	Pred. No.
1	216	8.0	323	1	FASA_BOVIN	FASL RECEPTOR PRECURSOR	6.03e-21	
2	191	7.0	335	1	FASA_HUMAN	FASL RECEPTOR PRECURSOR	3.59e-16	
3	189	7.0	474	1	TNRC_MOUSE	TUMOR NECROSIS FACTOR	8.49e-16	
4	187	6.9	349	1	VC22_VARV	PROTEIN C22/G28 HOMOLOG	2.00e-15	
5	185	6.8	427	1	NGFR_HUMAN	LOW-AFFINITY NERVE GROWTH FACTOR RECEPTOR	4.71e-15	
6	184	6.8	461	1	TNRI_PIG	TUMOR NECROSIS FACTOR	7.22e-15	
7	180	6.6	326	1	VT2_MXVL	TUMOR NECROSIS FACTOR	3.95e-14	
8	177	6.5	327	1	FASA_MOUSE	FASL RECEPTOR PRECURSOR	1.40e-13	
9	173	6.4	455	1	TNRI_HUMAN	TUMOR NECROSIS FACTOR	7.47e-13	
10	170	6.3	416	1	NGFR_CHICK	LOW-AFFINITY NERVE GROWTH FACTOR RECEPTOR	2.60e-12	
11	171	6.3	425	1	NGFR_RAT	LOW-AFFINITY NERVE GROWTH FACTOR RECEPTOR	1.72e-12	
12	166	6.1	325	1	VT2_SFVKA	TUMOR NECROSIS FACTOR	1.36e-11	
13	159	5.9	461	1	TNRI_RAT	TUMOR NECROSIS FACTOR	2.35e-10	
14	158	5.8	461	1	TNRI_MOUSE	TUMOR NECROSIS FACTOR	3.51e-10	
15	156	5.7	454	1	TNRI_MOUSE	TUMOR NECROSIS FACTOR	7.85e-10	
16	151	5.6	271	1	OX40_RAT	OX40 RECEPTOR PRECURSOR	5.75e-09	
17	151	5.6	272	1	OX40_MOUSE	OX40 RECEPTOR PRECURSOR	5.75e-09	
18	144	5.3	256	1	41BB_MOUSE	4-1BB LIGAND RECEPTOR	8.88e-08	
19	144	5.3	435	1	TNRC_HUMAN	LYMPHOTOXIN-BETA RECEPTOR	8.88e-08	
20	132	4.9	255	1	41BB_HUMAN	4-1BB LIGAND RECEPTOR	8.39e-06	
21	131	4.8	260	1	CD27_HUMAN	CD27 RECEPTOR PRECURSOR	1.21e-05	
22	130	4.8	277	1	OX40_HUMAN	OX40 RECEPTOR PRECURSOR	1.76e-05	
23	125	4.6	595	1	CD30_HUMAN	CD30 RECEPTOR PRECURSOR	1.08e-04	

24	125	4.6	719	1	YMP8_CAEEL	HYPOTHETICAL 82.6 KD P	1.08e-04
25	118	4.3	250	1	CD27_MOUSE	CD27 RECEPTOR PRECURSOR	1.29e-03
26	113	4.2	415	1	TNRC_MOUSE	LYMPHOTOXIN-BETA RECEPTOR	7.17e-03
27	110	4.1	277	1	CD40_HUMAN	CD40 RECEPTOR PRECURSOR	1.96e-02
28	109	4.0	1789	1	LMB1_DROME	LAMININ BETA-1 CHAIN P	2.73e-02
29	108	4.0	3133	1	HMCT_BOMMO	HOMOCYTIN PRECURSOR (H	3.79e-02
30	102	3.8	415	1	BOFH_BRAOL	POTATIVE TRANSCRIPTION	2.60e-01
31	104	3.8	431	1	SECY_BACSU	PREPROTEIN TRANSLOCASE	1.38e-01
32	104	3.8	569	1	HXT8_YEAST	HEXOSE TRANSPORTER EXT	1.38e-01
33	100	3.7	131	1	NU3M_CANPA	NADH-UBIQUINONE OXIDOR	4.86e-01
34	101	3.7	424	1	LEAF_ARATH	LEAFY PROTEIN	3.56e-01
35	101	3.7	502	1	K2W3_SHEEP	KERATIN, TYPE II MICRO	3.56e-01
36	100	3.7	549	1	COX1_TRYTB	CYTOCHROME C OXIDASE P	4.86e-01
37	100	3.7	628	1	RA21_SCHPO	DOUBLE-STRAND-BREAK RE	4.86e-01
38	98	3.6	85	1	OE18_NPVOV	OCCLUSION-DERIVED VIRU	9.98e-01
39	99	3.6	269	1	CD40_BOVIN	CD40 RECEPTOR PRECURSOR	6.61e-01
40	98	3.6	576	1	HXT4_YEAST	LOW-AFFINITY GLUCOSE T	8.98e-01
41	98	3.6	854	1	UBFK_HUMAN	UBIQUITIN CARBOXYL-TER	8.98e-01
42	99	3.6	974	1	MTSD_MESAU	MYOSIN HEAVY CHAIN, C	6.61e-01
43	98	3.6	1375	1	Y1P9_YEAST	HYPOTHETICAL 156.9 KD	8.98e-01
44	99	3.6	1935	1	MTSD_RAT	MYOSIN HEAVY CHAIN, C	6.61e-01
45	99	3.6	1935	1	MTSD_HUMAN	MYOSIN HEAVY CHAIN, C	6.61e-01

#### ALIGNMENTS

RESULT 1  
 ID FASA\_BOVIN STANDARD; PRT; 323 AA.  
 AC P51867;  
 DT 01-OCT-1996 (REL. 34, CREATED)  
 DT 01-OCT-1996 (REL. 34, LAST SEQUENCE UPDATE)  
 DT 01-NOV-1997 (REL. 35, LAST ANNOTATION UPDATE)  
 DE FASL RECEPTOR PRECURSOR (APOPTOSIS-MEDIATING SURFACE ANTIGEN FAS)  
 DE (APO-1 ANTIGEN) (CD95).  
 GN APT1 OR FAS.  
 OS BOS TAURUS (BOVINE).  
 OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;  
 OC EUTHERIA; ARTIODACTYLIA.  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE; 96226401.  
 RA YOO J., STONE R.T., BEATTIE C.W.;  
 RL DNA CELL BIOL. 15:227-234(1996).  
 CC -1- FUNCTION: RECEPTOR FOR A CYTOKINE LIGAND KNOWN AS FASL. THE  
 CC ADAPTOR MOLECULE FADD RECRUITS CASPASE-8 TO THE ACTIVATED  
 CC RECEPTOR. THE RESULTING AGGREGATE CALLED THE DEATH-INDUCING  
 CC SIGNALING COMPLEX (DISC) PERFORMS CASPASE-8 PROTEOLYTIC  
 CC ACTIVATION. ACTIVE CASPASE-8 INITIATES THE SUBSEQUENT CASCADE OF  
 CC CASPASES (ASPARTATE-SPECIFIC CYSTEINE PROTEASES) MEDIATING  
 CC APOPTOSIS. FAS- MEDIATED APOPTOSIS MAY HAVE A ROLE IN THE  
 CC INDUCTION OF PERIPHERAL TOLERANCE, IN THE ANTIGEN-STIMULATED  
 CC SUICIDE OF MATURE T-CELLS, OR BOTH (BY SIMILARITY).  
 CC -1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.  
 CC -1- DOMAIN: CONTAINS A DEATH DOMAIN INVOLVED IN THE BINDING OF FADD,  
 CC AND MAYBE TO OTHER CYTOSOLIC ADAPTOR PROTEINS.  
 CC -1- SIMILARITY: CONTAINS A LA-NGFR/TNFR-TYPE CYSTEINE-RICH REGION.  
 DR EMBL; U04794; G1262193; -.  
 DR PROSITE; PS00652; TNFR\_NGFR\_1; 2.  
 DR PROSITE; PS00650; TNFR\_NGFR\_2; 2.  
 DR PROSITE; PS00017; DEATH\_DOMAIN; 1.  
 KW APOPTOSIS; RECEPTOR; GLYCOPROTEIN; TRANSMEMBRANE; REPEAT; SIGNAL.  
 FT SIGNAL 1 16  
 FT CHAIN 17 323  
 FT DOMAIN 17 170  
 FT TRANSMEM 171 188  
 FT DOMAIN 189 323  
 FT DOMAIN 45 163  
 FT REPEAT 45 80  
 FT REPEAT 81 124  
 FT REPEAT 125 163  
 FT DOMAIN 238 306  
 SQ SEQUENCE 323 AA; 36445 MW; DA5A2A59 CRC32;

FT	SIGNAL	1	22	
FT	CHAIN	23	474	TUMOR NECROSIS FACTOR RECEPTOR 2
FT	DOMAIN	23	258	EXTRACELLULAR (POTENTIAL).
FT	TRANSMEM	259	288	POTENTIAL.
FT	DOMAIN	289	474	CYTOSOLIC (POTENTIAL).
FT	DOMAIN	39	203	4 X TNFR-CYS.
FT	REPEAT	39	77	TNFR-CYS 1.
FT	REPEAT	78	119	TNFR-CYS 2.
FT	REPEAT	120	164	TNFR-CYS 3.
FT	REPEAT	165	203	TNFR-CYS 4.

[illegible]

Query Match 6.88; Score 184; DB 1; Length 461;  
Best Local Similarity 36.3%; Pred. No. 7.22e-15;  
Matches 33; Conservative 17; Mismatches 32; Indels 9; Gaps 7;

Db 81 CRECDNGT-PTASENHLTQCLSCSKRSEMSQVEISPTVDRTVCGCRKNQYR-KYWE 138

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RESULT      8
ID  FASA_MOUSE      STANDARD;      PRT;   327 AA.
AC  P25446;
DT  01-MAY-1992 (REL. 22, CREATED)
DT  01-MAY-1992 (REL. 22, LAST SEQUENCE UPDATE)
DT  01-NOV-1997 (REL. 35, LAST ANNOTATION UPDATE)
DE  FAS RECEPTOR PRECURSOR (APOPTOSIS-MEDIATING SURFACE ANTIGEN FAS)
GN  (APO-1 ANTIGEN) (CD95).
SW  APT1 OR FAS.
OS  MUS MUSCULUS (MOUSE).
OC  EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
OC  EUTHERIA; RODENTIA.
RN  111

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INSULT 9  
 ID TNRI\_HUMAN STANDARD; PRT; 455 AA.  
 AC P19438;  
 DT 01-FEB-1991 (REL. 17, CREATED)  
 DT 01-FEB-1991 (REL. 17, LAST SEQUENCE UPDATE)  
 DT 01-NOV-1997 (REL. 35; LAST ANNOTATION UPDATE)  
 DE TUMOR NECROSIS FACTOR RECEPTOR 1 PRECURSOR (TUMOR NECROSIS FACTOR  
 DE BINDING PROTEIN 1) (TNFRI) (P60) (TNF-RI) (P55) (CD120A).  
 GN TNFRI OR TNFR.  
 OS HOMO SAPIENS (HUMAN).  
 CC EURKARYOTA; METAQOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;  
 CC EUTHERIA; PRIMATES.  
 RN [1]  
 RX SEQUENCE FROM N.A.  
 RC TISSUE=PLACENTA;  
 RX MEDLINE: 90235285.  
 RA SCHALL T.J., LEWIS M., KOLLER K.J., LEE A., RICE G.C., WONG G.H.W.,  
 RA GETANAGA T., GRANGER G.A., LENTZ R., RAAB R., KOHR W.J., GOEDEL D.V.;  
 RL CELL 61:361-370(1990).  
 RN [2]  
 RX SEQUENCE FROM N.A.  
 RX MEDLINE: 90235284.  
 RA LOETSCHER H., PAN Y.-C.E., LAHM H.-W., GENTZ R., BROCKHAUS M.,  
 RA TABUCHI H., LESSLAUER W.;  
 RL CELL 61:351-359(1990).  
 RN [3]  
 RX SEQUENCE FROM N.A., AND SEQUENCE OF 41-53; 110-124 AND 199-201.  
 RX MEDLINE: 91060021.  
 RA NOPHAR T.J., KEMPEL D., BRAKEBUSCH C., ENGELMANN H., ZWANG R.,  
 RA ADERKA D., HOLTZMAN R., WALLACH D.;  
 RL EMBO J. 9:3269-3278(1990).  
 RN [4]  
 RX SEQUENCE FROM N.A.  
 RX MEDLINE: 91090481.  
 RA HIMMER A., MAURER-POGY I., KROENKE M., SCHEURICH P., PFIZENMAIER K.,  
 RA LANTZ M., OLSSON I., HAUPTMANN R., STRATOWA C., ADOLF G.R.;  
 RL DNA CELL BIOL. 9:705-715(1990).  
 RN [5]  
 RX SEQUENCE FROM N.A.  
 RC TISSUE=PLACENTA;  
 RX MEDLINE: 91017509.  
 RA GHAI P.W., BARRETT K., CHANTRY D., TURNER M., FELDMAN M.;  
 RL PROC. NATL. ACAD. SCI. U.S.A. 87:7380-7384(1990).  
 RN [6]  
 RX SEQUENCE FROM N.A.  
 RX MEDLINE: 92250049.  
 RA FUCHS P., STEHL S., DWORZAK M., HIMMLER A., AMBROS P.F.;  
 RL GENOMICS 13:219-224(1992).  
 RN [7]  
 RX SEQUENCE OF 41-45.  
 RX MEDLINE: 90110215.  
 RA ENGELMANN H., NOVICK D., WALLACH D.;  
 RL J. BIOL. CHEM. 265:1531-1536(1990).  
 RN [8]  
 RX X-RAY CRYSTALLOGRAPHY (2.85 ANGSTROMS) OF 30-211.  
 RX MEDLINE: 93258809.  
 RA BANNER D.W., D'ARCY A., JAMES W., GENTZ R., SCHOENFELD H.-J.,  
 RA BROGER C., LOETSCHER H., LESSLAUER W.;  
 RL CELL 73:431-445(1993).  
 RN [9]  
 RX X-RAY CRYSTALLOGRAPHY (1.85 ANGSTROMS) OF 41-202.  
 RX MEDLINE: 97094982.  
 RA NAIMSITH J.H., DEVINE T.Q., KHONO R., SPRANG S.R.;  
 RL STRUCTURE 4:1251-1262(1996).  
 CC -1- FUNCTION: RECEPTOR FOR TNF-ALPHA. THE ADAPTOR MOLECULE FADD  
 CC RECRUITS CASPASE-8 TO THE ACTIVATED RECEPTOR. THE RESULTING  
 CC AGGREGATE CALLED THE DEATH-INDUCING SIGNALING COMPLEX (DISC)  
 CC PERFORMS CASPASE-8 PROTEOLYTIC ACTIVATION WHICH INITIATES THE  
 CC SUBSEQUENT CASCADE OF CASPASES (ASPARTATE-SPECIFIC CYSTEINE  
 CC PROTEASES) MEDIATING APOPTOSIS.  
 CC -1- SUBUNIT: TNF BINDING TO THE EXTRACELLULAR DOMAIN OF TNFRI LEADS TO  
 CC HOMODIMERIZATION. ONCE AGGREGATED THE RECEPTORS DEATH DOMAINS

CC PROVIDE A NOVEL MOLECULAR INTERFACE THAT INTERACTS SPECIFICALLY  
 CC WITH THE DEATH DOMAIN OF TRADD. VARIOUS TRADD-INTERACTING  
 CC PROTEINS SUCH AS TRAFs, RIP AND POSSIBLY FADD, ARE RECRUITED TO  
 CC TNFR1 COMPLEX BY THEIR ASSOCIATION WITH TRADD. THIS COMPLEX  
 CC ACTIVATES AT LEAST TWO DISTINCT SIGNALING CASCADES, APOPTOSIS AND  
 CC NF-KAPPA B SIGNALING.  
 CC -1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.  
 CC -1- SIMILARITY: CONTAINS A LA-NGFR/TNFR-TYPE CYSTEINE-RICH REGION.  
 DR EMBL: M55131; G37224; -.  
 DR EMBL: M33294; G339745; -.  
 DR EMBL: M58286; G339754; -.  
 DR EMBL: M63121; G339756; -.  
 DR EMBL: M75866; G339750; -.  
 DR EMBL: M75864; G339750; JOINED.  
 DR EMBL: M75865; G339750; JOINED.  
 DR EMBL: M50275; G339760; -.  
 DR EMBL: A21522; G579600; -.  
 DR PIR: A34899; G0RUT1.  
 DR PIR: A35010; A35010.  
 DR PIR: S12057; S12057.  
 DR PIR: A38208; A38208.  
 DR PDB: 1TNR; 31-JUL-94.  
 DR PDB: 1NCF; 07-DEC-95.  
 DR PDB: 1EAT; 11-JAN-97.  
 DR MIM: 191190; -.  
 DR PROSITE: PS00652; TNFR\_NGFR\_1; 3.  
 DR PROSITE: PS50050; TNFR\_NGFR\_2; 3.  
 DR PROSITE: PS50017; DEATH\_DOMAIN; 1.  
 KW RECEPTOR; TRANSMEMBRANE; GLYCOPROTEIN; REPEAT; SIGNAL; APOPTOSIS;  
 NW 3D-STRUCTURE.  
 FT SIGNAL 1 21  
 FT CHAIN 22 455 TUMOR NECROSIS FACTOR RECEPTOR 1.  
 FT CHAIN 41 291 TUMOR NECROSIS FACTOR BINDING PROTEIN 1.  
 FT DOMAIN 22 211 EXTRACELLULAR (POTENTIAL).  
 FT TRANSMEM 212 234 POTENTIAL.  
 FT DOMAIN 235 455 CYTOPLASMIC (POTENTIAL).  
 FT DOMAIN 43 196 4 X TNFR-CYS.  
 FT REPEAT 43 82 TNFR-CYS 1.  
 FT REPEAT 83 125 TNFR-CYS 2.  
 FT REPEAT 126 166 TNFR-CYS 3.  
 FT REPEAT 167 196 TNFR-CYS 4.  
 FT DOMAIN 356 441 DEATH DOMAIN.  
 FT DISULFID 44 58  
 FT DISULFID 59 72  
 FT DISULFID 62 81  
 FT DISULFID 84 99  
 FT DISULFID 102 117  
 FT DISULFID 105 125  
 FT DISULFID 127 143  
 FT DISULFID 146 158  
 FT DISULFID 149 166  
 FT DISULFID 168 179  
 FT DISULFID 182 191  
 FT DISULFID 185 195  
 FT CARBOHYD 54 54 POTENTIAL.  
 FT CARBOHYD 145 145 POTENTIAL.  
 FT CARBOHYD 151 151 POTENTIAL.  
 FT CONFLICT 412 412 MISSING (IN REF. 4).  
 FT CONFLICT 443 446 GPAA -> APP (IN REF. 4).  
 SQ SEQUENCE 455 AA; 50494 MW; C0B0A06F CRC32;  
 Query Match 6.44; Score 173; DB 1; Length 455;  
 Best Local Similarity 37.14; Pred. No. 7.47e-13;  
 Matches 33; Conservative 12; Mismatches 37; Indels 7; Gaps 6;  
 Db 81 CRECEG-SPTASENHLRCLSCSKCRKMGQVSEISCTVDORTVCCGRKNQYRHTWSN 139  
 | | | : | : | | | | | | | | | | : | : |  
 Qy 96 NCPTGEGVDTTASNNLPSCLICTVC-KS-GQTNKSCSTTTDRTVCCQCEGSGPDKNSE 153  
 Db 140 LQFCFNCSL-CLNGTVHLS-C0RKQNTVC 166  
 : | | | | | : | : | : |  
 Qy 154 M-CRTRCTCGPRHNVKVSNCPTPRDINC 180

RESULT 10  
 ID NGFR\_CHICK STANDARD; PRT; 416 AA.  
 AC P18519;  
 DT 01-NOV-1990 (REL. 16, CREATED)  
 DT 01-NOV-1990 (REL. 16, LAST SEQUENCE UPDATE)  
 DT 01-NOV-1997 (REL. 35, LAST ANNOTATION UPDATE)  
 DE LOW-AFFINITY NERVE GROWTH FACTOR RECEPTOR PRECURSOR (NGF RECEPTOR)  
 DE (GP80-LNGFR).  
 GN NGFR.  
 OS GALLUS GALLUS (CHICKEN).  
 OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; AVES; NEOGNATHAE;  
 OC OCCELLIFORMES.  
 RN [1]  
 RC SEQUENCE FROM N.A.  
 RC TISSUE=BRAIN;  
 RX MEDLINE; 90166579.  
 RA LARGE T.H., WESKAMP G., HELDER J.C., RADEKE M.J., Misko T.P.,  
 RA SHOOTER E.M., REICHARDT L.P.;  
 RL NEURON 2:1123-1134(1989).  
 RN [2]  
 RP SEQUENCE OF 21-416 FROM N.A.  
 RX MEDLINE; 90152140.  
 RA HEUER J.G., FATEMI-MAINIE S., WHEELER E.F., BOTHWELL M.;  
 RL DEV. BIOL. 137:287-304(1990).  
 CC -1- FUNCTION: LOW AFFINITY RECEPTOR WHICH CAN BIND TO NGF, BDNF,  
 CC NT-3, AND NT-4.  
 CC -1- SUBUNIT: NGF RECEPTOR CAN FORM A HOMODIMER THROUGH DISULFIDE  
 CC BOND FORMATION.  
 CC -1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.  
 CC -1- PTM: N- AND O-GLYCOSYLATED AND IS PHOSPHORYLATED ON SERINE.  
 CC -1- SIMILARITY: CONTAINS A LA-NGFR/TNFR-TYPE CYSTEINE-RICH REGION.  
 DR PIR: JN0006; JN0006.  
 DR PIR: A60504; A60504.  
 DR PROSITE: PS00652; TNFR\_NGFR\_1; 3.  
 DR PROSITE: PS50050; TNFR\_NGFR\_2; 3.  
 DR PROSITE: PS50017; DEATH\_DOMAIN; 1.  
 KW RECEPTOR; NEUROGENESIS; TRANSMEMBRANE; GLYCOPROTEIN; REPEAT;  
 KW PHOSPHORYLATION; SIGNAL.  
 FT SIGNAL 1 19 POTENTIAL.  
 FT CHAIN 20 416 NGF RECEPTOR.  
 FT DOMAIN 29 239 EXTRACELLULAR (POTENTIAL).  
 FT TRANSMEM 240 261 POTENTIAL.  
 FT DOMAIN 262 416 CYTOPLASMIC (POTENTIAL).  
 FT DOMAIN 23 181 4 X TNFR-CYS.  
 FT REPEAT 23 57 TNFR-CYS 1.  
 FT REPEAT 58 100 TNFR-CYS 2.  
 FT REPEAT 101 140 TNFR-CYS 3.  
 FT REPEAT 141 181 TNFR-CYS 4.  
 FT DOMAIN 188 236 SER/THR-RICH.  
 FT DOMAIN 333 410 DEATH DOMAIN.  
 FT DISULFID 24 35 BY SIMILARITY.  
 FT DISULFID 36 49 BY SIMILARITY.  
 FT DISULFID 39 56 BY SIMILARITY.  
 FT DISULFID 59 75 BY SIMILARITY.  
 FT DISULFID 78 91 BY SIMILARITY.  
 FT DISULFID 81 99 BY SIMILARITY.  
 FT DISULFID 101 114 BY SIMILARITY.  
 FT DISULFID 117 130 BY SIMILARITY.  
 FT DISULFID 120 138 BY SIMILARITY.  
 FT DISULFID 141 156 BY SIMILARITY.  
 FT DISULFID 159 172 BY SIMILARITY.  
 FT DISULFID 162 180 BY SIMILARITY.  
 FT CARBOHYD 52 52 POTENTIAL.  
 FT CONFLICT 36 36 C -> Y (IN REF. 2).  
 FT CONFLICT 173 173 T -> K (IN REF. 2).  
 FT CONFLICT 276 276 N -> S (IN REF. 2).  
 FT CONFLICT 396 396 K -> R (IN REF. 2).  
 SQ SEQUENCE 416 AA; 44654 MW; 4D3F086A CRC32;  
 Query Match 6.34; Score 170; DB 1; Length 416;  
 Best Local Similarity 30.64; Pred. No. 2.60e-12;  
 Matches 26; Conservative 17; Mismatches 40; Indels 2; Gaps 2;

Query Match 6.18; Score 166; DB 1; Length 325;  
Best Local Similarity 33.0%; Pred. No. 1.36e-11;  
Matches 29; Conservative 20; Mismatches 34; Indels 5; Gaps 4;

Db 61 CSPCEDGT-FTASTNHAPACVSCRGCTGHTLSESPQCDTRHVCNCSTGYNCLLKQNG 119

Qy 96 CNPCTGVDYTIASNNPLSCILC-TVGKSGQTKKSSCTTTRDVCQCKGCSFQDKNSPM 154

Db 120 CRICAPQTKCPAGVG-VSGHTRAGDTLC 146  
| | | | | | | | | | | | | | | |

Qy 155 CRIC-RTGCPGRGVKVSNCPTPRSDIKC 180

RESULT 13

ID TNRI\_RAT STANDARD: PRT: 461 AA.

AC P22934;

DT 01-AUG-1991 (REL. 19, CREATED)

DT 01-MAR-1992 (REL. 21, LAST SEQUENCE UPDATE)

DT 01-NOV-1997 (REL. 35, LAST ANNOTATION UPDATE)

DE TUMOR NECROSIS FACTOR RECEPTOR 1 PRECURSOR (P60) (TNF-R1) (P55).

GN TNFR1 OR TNFR-1.

OS RATTUS NORVEGICUS (RAT).

OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;

OC EUTHERIA; RODENTIA.

RN [1]

RP SEQUENCE FROM N.A.

RX MEDLINE; 91090841.

RA HIMMLER A., MAURER-FOGY I., KROENKE M., SCHEURICH P., PILZENMAIER K.,  
LAUTZ M., OLSSON I., HAUPTMANN R., STRATOWA C., ADOLF G.R.;

RL DNA CELL BIOL. 9:705-715(1990).

CC -1- FUNCTION: RECEPTOR FOR TNF-ALPHA. THE ADAPTOR MOLECULE FADD  
RECRUITS CASPASE-8 TO THE ACTIVATED RECEPTOR. THE RESULTING  
AGGREGATE CALLED THE DEATH-INDUCING SIGNALING COMPLEX (DISC)  
PERFORMS CASPASE-8 PROTEOLYTIC ACTIVATION WHICH INITIATES THE  
SUBSEQUENT CASCADE OF CASPASES (ASPARTATE-SPECIFIC CYSTEINE  
PROTEASES) MEDIATING APOPTOSIS (BY SIMILARITY).

CC -1- SUBUNIT: TNF BINDING TO THE EXTRACELLULAR DOMAIN OF TNFR1 LEADS TO  
HOMOTRIMERIZATION. ONCE AGGREGATED THE RECEPTORS DEATH DOMAINS  
PROVIDE A NOVEL MOLECULAR INTERFACE THAT INTERACTS SPECIFICALLY  
WITH THE DEATH DOMAIN OF TRADD. VARIOUS TRADD-INTERACTING  
PROTEINS SUCH AS TRAFS, RIP AND POSSIBLY FADD, ARE RECRUITED TO  
TNFR1 COMPLEX BY THEIR ASSOCIATION WITH TRADD. THIS COMPLEX  
ACTIVATES AT LEAST TWO DISTINCT SIGNALING CASCADES, APOPTOSIS AND  
NF-KAPPA B SIGNALING (BY SIMILARITY).

CC -1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.

CC -1- SIMILARITY: CONTAINS A LA-NGFR/TNFR-TYPE CYSTEINE-RICH REGION.

DR EMBL; M53122; G207362; .

DR PIR; B36555; B36555.

DR HSSP; P19438; TNFR.

DR PROSITE; P500652; TNFR\_NGFR\_1; 3.

DR PROSITE; P500050; TNFR\_NGFR\_2; 3.

DR PROSITE; P500017; DEATH\_DOMAIN; 1.

KW RECEPTOR; TRANSMEMBRANE; GLYCOPROTEIN; REPEAT; SIGNAL; APOPTOSIS.

FT SIGNAL 1 21 POTENTIAL.

FT CHAIN 22 455 TUMOR NECROSIS FACTOR RECEPTOR 1.

FT DOMAIN 22 211 EXTRACELLULAR (POTENTIAL).

FT TRANSMEM 212 234 POTENTIAL.

FT DOMAIN 235 461 CYTOPLASMIC (POTENTIAL).

FT DOMAIN 43 196 4 X TNFR-CYS.

FT REPEAT 43 82 TNFR-CYS 1.

FT REPEAT 83 125 TNFR-CYS 2.

FT REPEAT 126 166 TNFR-CYS 3.

FT REPEAT 167 196 TNFR-CYS 4.

FT DOMAIN 363 448 DEATH DOMAIN.

FT DISULFID 44 58 BY SIMILARITY.

FT DISULFID 59 72 BY SIMILARITY.

FT DISULFID 62 81 BY SIMILARITY.

FT DISULFID 84 99 BY SIMILARITY.

FT DISULFID 102 117 BY SIMILARITY.

FT DISULFID 105 125 BY SIMILARITY.

FT DISULFID 127 143 BY SIMILARITY.

FT DISULFID 146 158 BY SIMILARITY.

FT DISULFID 149 166 BY SIMILARITY.

FT DISULFID 168 179 BY SIMILARITY.

FT DISULFID 182 191 BY SIMILARITY.

FT DISULFID 185 195 BY SIMILARITY.

FT CARBOHYD 54 54 POTENTIAL.

FT CARBOHYD 151 151 POTENTIAL.

FT CARBOHYD 201 201 POTENTIAL.

SQ SEQUENCE 461 AA; 50969 MW; 82P68B08 CRC32;

Query Match 5.9%; Score 159; DB 1; Length 461;  
Best Local Similarity 30.0%; Pred. No. 2.35e-10;  
Matches 27; Conservative 16; Mismatches 40; Indels 7; Gaps 6;

Db 81 CEVCDKGT-PTASQNHVROCLSKCTCRKMFQVEISPKADMDTVCCCKNFOQRTLSST 139  
| | | | | | | | | | | | | | | |

Qy 96 CNPCTGVDYTIASNNPLSCILC-TVGKSGQTKKSSCTTTRDVCQCKGCSFQDKNSP 152

Db 140 HFQCVOC-SPCFNVTGTVI-CRKEQNTVCN 167  
| | | | | | | | | | | | | | | |

Qy 153 EM-CRTRCGRGCPGRGVKVSNCPTPRSDIKC 181

RESULT 14

ID TNRI\_HUMAN STANDARD: PRT: 461 AA.

AC P20333;

DT 01-FEB-1991 (REL. 17, CREATED)

DT 01-AUG-1991 (REL. 19, LAST SEQUENCE UPDATE)

DT 01-NOV-1997 (REL. 35, LAST ANNOTATION UPDATE)

DE TUMOR NECROSIS FACTOR RECEPTOR 2 PRECURSOR (TUMOR NECROSIS FACTOR  
BINDING PROTEIN 2) (TNF1) (P80) (TNF-R2) (P75) (CD120B).

GN TNFR2 OR TNFR.

OS HOMO SAPIENS (HUMAN).

OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;

OC EUTHERIA; PRIMATES.

RN [1]

RP SEQUENCE FROM N.A.

RX MEDLINE; 90260639.

RA SMITH C.A., DAVIDS T., ANDERSON D., SOLAM L., BECKMANN M.P., JERRY R.,  
DOWER S.K., COSMAN D., GOODWIN R.G.;

RL SCIENCE 248:1019-1023(1990).

RN [2]

RP SEQUENCE FROM N.A.

RX MEDLINE; 91045951.

RA KONO T., BREWER M.T., BAKER S.L., SCHWARTZ P.E., KING M.W.,  
HALE K.K., SQUIRES C.H., THOMPSON R.C., VANNICE J.L.;

RL PROC. NATL. ACAD. SCI. U.S.A. 87:8351-8355(1990).

RN [3]

RP SEQUENCE FROM N.A.

RX MEDLINE; 96299745.

RA BELTINGER C.P., WHITE P.S., MARIS J.M., SULMAN E.P., JENSEN S.J.,  
LEPASLIER D., STALLARD B.J., GOEDEL D.V., DESAUVAGE F.J.;

RA BRODEUR G.M.;

RL GENOMICS 35:94-100(1996).

RN [4]

RP SEQUENCE OF 116-461 FROM N.A., AND PARTIAL SEQUENCE.

RX MEDLINE; 90349572.

RA HELLER R.A., SONG K., ONASCH M.A., FISCHER W.H., CHANG D.,  
RINGOLD G.M.;

RL PROC. NATL. ACAD. SCI. U.S.A. 87:6151-6155(1990).

RN [5]

RP SEQUENCE OF 27-31.

RX MEDLINE; 90110215.

RA ENGELMANN H., NOVICK D., WALLACH D.;

RL J. BIOL. CHEM. 265:1531-1536(1990).

RN [6]

RP SEQUENCE OF 22-40; 65-69; 136-141; 300-306 AND 346-362.

RX MEDLINE; 91056048.

RA LOETSCHER H., SCHLAGER E.J., LAHM H.-W., PAN Y.-C.E., LESSLAUER W.,  
BROCKHAUS M.;

RL J. BIOL. CHEM. 265:20131-20138(1990).

RN [7]

RP CHARACTERIZATION.

RX MEDLINE; 93016040.

RA PENNICA D., LAM V.T., MIZE N.X., WEBER R.F., LEWIS M., FENDLY B.M.,  
LIPARI M.T., GOEDEL D.V.;

RL J. BIOL. CHEM. 267:21172-21178(1992).

CC -1- FUNCTION: RECEPTOR FOR TNF-ALPHA. HIGH AFFINITY FOR TNF-ALPHA AND  
APPROXIMATELY 5-FOLD LOWER AFFINITY FOR TNF-BETA.

CC -1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.

CC -1- PTM: PHOSPHORYLATED; MAINLY ON SERINE RESIDUES WITH A VERY LOW



TNFR1 OR TNFR-1.  
 OS MUS MUSCULUS (MOUSE).  
 OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;  
 OC EUTHERIA; RODENTIA.  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE: 9118785.  
 RA LEWIS M., TARTAGLIA L.A., LEE A., BENNETT G.L., RICE G.C.,  
 RA WONG G.H., CHEN E.Y., GOEDDEL D.V.  
 RL PROC. NATL. ACAD. SCI. U.S.A. 88:2830-2834 (1991).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE: 91246158.  
 RA GOODWIN R.G., ANDERSON D., JERZY R., DAVIS T., BRANNAN C.I.,  
 RA COPELAND N.G., JENKINS N.A., SMITH C.A.;  
 RL MOL. CELL. BIOL. 11:3020-3026 (1991).  
 RN [3]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE: 91855014.  
 RA BARRETT K., TAYLOR-FISHWICK D.A., COPE A.P., KISSONERGHIS A.M.,  
 RA GRAY P.W., FELDHAUS M., FOXWELL B.M.J.;  
 RL EUR. J. IMMUNOL. 21:1649-1656 (1991).  
 RN [4]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE-SPLEEN;  
 RX MEDLINE: 92039815.  
 RA ROTHE J.G., BROCKHAUS M., GENTZ R., LESSLAUER W.;  
 RL IMMUNOGENETICS 34:338-340 (1991).  
 RN [5]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE: 94245292.  
 RA BEBO B.F., LINTHICUM D.S.;  
 RL IMMUNOGENETICS 39:450-451 (1994).  
 RN [6]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE: 93156721.  
 RA ROTHE J., BLOETHEMAN H., GENTZ R., LESSLAUER W., STEINMETZ M.;  
 RL MOL. IMMUNOL. 30:165-175 (1993).  
 CC -1- FUNCTION: RECEPTOR FOR TNF-ALPHA. THE ADAPTOR MOLECULE FADD  
 CC AGGREGATES CASPASE-8 TO THE ACTIVATED RECEPTOR. THE RESULTING  
 CC COMPLEXES CALLED THE DEATH-INDUCING SIGNALING COMPLEX (DISC)  
 CC PERFORMS CASPASE-8 PROTEOLYTIC ACTIVATION WHICH INITIATES THE  
 CC SUBSEQUENT CASCADE OF CASPASES (ASPARTATE-SPECIFIC CYSTEINE  
 CC PROTEASES) MEDIATING APOPTOSIS (BY SIMILARITY).  
 CC -1- SUBUNIT: TNF BINDING TO THE EXTRACELLULAR DOMAIN OF TNFR1 LEADS TO  
 CC HOMOTRIMERIZATION. ONCE AGGREGATED THE RECEPTORS DEATH DOMAINS  
 CC PROVIDE A NOVEL MOLECULAR INTERFACE THAT INTERACTS SPECIFICALLY  
 CC WITH THE DEATH DOMAIN OF TRADD. VARIOUS TRADD-INTERACTING  
 CC PROTEINS SUCH AS TRAFs, RIP AND POSSIBLY FADD, ARE RECRUITED TO  
 CC TNFR1 COMPLEX BY THEIR ASSOCIATION WITH TRADD. THIS COMPLEX  
 CC ACTIVATES AT LEAST TWO DISTINCT SIGNALING CASCADES, APOPTOSIS AND  
 CC NF-KAPPA B SIGNALING (BY SIMILARITY).  
 CC -1- SUBCELLULAR LOCATION: TYPE 1 MEMBRANE PROTEIN.  
 CC -1- SIMILARITY: CONTAINS A LA-NGFR/TNFR-TYPE CYSTEINE-RICH REGION.  
 DR ENBL: M60468; G199826; -.  
 DR ENBL: M59377; G202097; -.  
 DR ENBL: X59238; G53579; -.  
 DR ENBL: X57796; G54849; -.  
 DR ENBL: L26349; G430733; -.  
 DR ENBL: M76656; G202102; -.  
 DR ENBL: M88067; G202102; JOINED.  
 DR ENBL: M76655; G202102; JOINED.  
 DR PIR: A38634; GQMST1.  
 DR PIR: I16677; I16677.  
 DR PIR: S19021; I19021.  
 DR HSSP: P19438; 1TNF.  
 DR MGD: MGI:98781; TNFR1.  
 DR PROSITE: PS00652; TNFR\_NGFR\_1; 3.  
 DR PROSITE: PS00050; TNFR\_NGFR\_2; 3.  
 DR PROSITE: PS00017; DEATH\_DOMAIN; 1.  
 KW RECEPTOR; TRANSMEMBRANE; GLYCOPROTEIN; REPEAT; SIGNAL; APOPTOSIS.  
 FT SIGNAL 1 21 POTENTIAL.  
 FT CHAIN 22 454 TUMOR NECROSIS FACTOR RECEPTOR 1.

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FT DOMAIN      22  212  EXTRACELLULAR (POTENTIAL).
FT TRANSMEM    213  235  POTENTIAL.
FT DOMAIN      236  454  CYTOPLASMIC (POTENTIAL).
FT DOMAIN      43  196  4 X TNFR-CYS.
FT REPEAT      43  82   TNFR-CYS 1.
FT REPEAT      83  125  TNFR-CYS 2.
FT REPEAT     126  166  TNFR-CYS 3.
FT REPEAT     167  196  TNFR-CYS 4.
FT DOMAIN     356  441  DEATH DOMAIN.
FT DISULFID    44  58   BY SIMILARITY.
FT DISULFID    59  72   BY SIMILARITY.
FT DISULFID    62  81   BY SIMILARITY.
FT DISULFID    84  99   BY SIMILARITY.
FT DISULFID   102  117  BY SIMILARITY.
FT DISULFID   105  125  BY SIMILARITY.
FT DISULFID   127  143  BY SIMILARITY.
FT DISULFID   146  158  BY SIMILARITY.
FT DISULFID   149  166  BY SIMILARITY.
FT DISULFID   168  179  BY SIMILARITY.
FT DISULFID   182  191  BY SIMILARITY.
FT DISULFID   185  195  BY SIMILARITY.
FT CARBOHYD    54  54   POTENTIAL.
FT CARBOHYD   151  151  POTENTIAL.
FT CARBOHYD   202  202  POTENTIAL.
FT CONFLICT    394  394  R -> G (IN REF. 6).
SQ SEQUENCE   454 AA;  50129 MW;  4B6EC09 CRC32;

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Query Match      5.7%; Score 156; DB 1; Length 454;
Best Local Similarity 30.8%; Pred. No. 7.85e-10;
Matches 32; Conservative 17; Mismatches 44; Indels 11; Gaps 11;

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Db  71 DCPSPG-R-D-T-VCRCEKGT-FTASQVLRCLSKTCRKEMSQVEISPCQADKDTVC 125
    :||: : | : | | | | : | : | | | | | : | : | : | |||
Qy  82 ECPAGSHRSEYTGACNPCTEGVDYTIASNNLPSCLLCTVC-KS-GQTNKSSCTTTRDTVC 139

Db  126 GCKENQFQRYLSETHFQCVDG-SPCFNGVTYIP-CKETQNTVCN 167
    | | : | | : | | : | : | : | : | : | : | : | : | : |
Qy  140 QCEKGSFQD-KNSPEM-CRTCRTGCPAGWVYVSNCTPRSDINCK 181

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Search completed: Thu May 14 16:47:55 1998
Job time : 22 secs.

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MORC (TM)

Db 151 ttttntnattttttgtagagacggggttcaccctgttgccaggctggtctcaaaactc 210  
||||| |||| | |||||  
Cp 1716 TTTTTCCTTTTAAATGAGATGGAGTTTCACTGTGTGATGAGGCCTGGTCTCAAAC TC 1657

Db 211 ctgaactcaagaactctgccacctaaacctctcaaagtctgcattacaagcatgacc 270

PT Transgenic plants co-expressing 2-5A-dependent RNase and 2-5A  
PT synthetase - have increased resistance to viral infection esp. to  
PT tobacco mosaic virus, tobacco etch virus or alfalfa mosaic virus  
PS Disclosure; Page 145-146; 189pp; English.

CC A cDNA clone (T59650) codes for human dsRNA-dependent protein  
CC kinase (PKR) (W12705), an antiviral protein that is believed to  
CC phosphorylate the alpha subunit of translation factor eIF2-alpha.

CC which indirectly inhibits protein synthesis initiation. Novel  
 CC transgenic plants, such as transgenic tobacco, express (together or  
 CC alone) the PKR, human 2-5A synthetase (see also T59645) and human  
 CC or mouse 2-5A-dependent RNase (see also T59648-49). When the  
 CC plants are exposed to tobacco mosaic virus, tobacco etch virus and  
 CC alfalfa mosaic virus, necrotic local lesions occur instead of  
 CC typical systemic infections.  
 SQ Sequence 2562 BP; 842 A; 478 C; 501 G; 741 T;

Query Match 4.0%; Score 83; DB 28; Length 2562;  
 Best Local Similarity 83.24; Pred. No. 1.01e-37;  
 Matches 104; Conservative 0; Mismatches 21; Indels 0; Gaps 0;

Db 2223 tttttgtgtttttaataagacagaggtttccaccatgtggcaggctggtctcaaacctc 2282  
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

Cp 1715 TTTTTCCTTTTAAATTGAGATGGAGTTTCACCTGTGTGTATGAGGCTGGTCTCAAACTCC 1656

Db 2283 tgacctcaagtaataccactgctcgtcgtcccaaaagtctgggtatcacaggatgagcc 2342  
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

Cp 1655 CGAGCTCAGCAATCCACCTGCTCAGCCTATCAAGTCTGGGATTACAGGCATGAGCC 1596

Db 2343 accgc 2347  
 |||||

Cp 1595 ACCGC 1591

RESULT 5  
 ID T03903 standard; DNA; 2562 BP.  
 AC T03903;  
 DT 27-JAN-1996 (first entry)  
 DE Human p68 kinase mRNA (PKR) coding sequence.  
 KW PK68; p68 kinase; mrPK68; ss.  
 OS Homo sapiens.  
 PN M0952245-A.  
 PD 24-AUG-1995.  
 PF 16-FEB-1995; U02058.  
 PR 18-FEB-1994; US-198973.  
 PA (CLEV-) CLEVELAND CLINIC FOUND.  
 PI Sengupta DN, Silverman RH;  
 DR WPI; 95-302493/39.  
 PT New transgenic plants resistant to viral infection contg. 2-5A-dependent  
 PT RNase - useful in developing products useful in gene therapy against  
 PT viral disease and cancer.  
 PS Claim 4; Figure 18; 196pp; English.  
 CC PKR (PK68) is a lysine - arginine mutant PKR (mrPK68). The mutant  
 CC PKR protein binds to dsRNA but has no kinase activity. A transgenic  
 CC plant is claimed which includes the nts in T03903 or any part of  
 CC this sequence which contains the complete or partial coding  
 CC sequence for PKR or the ds RNA binding domain of PKR. The  
 CC translation product of the complete coding sequence for human  
 CC p68 kinase mRNA (PKR) is given in R82663.  
 SQ Sequence 2562 BP; 842 A; 478 C; 501 G; 740 T;

Query Match 4.0%; Score 83; DB 15; Length 2562;  
 Best Local Similarity 83.24; Pred. No. 1.01e-37;  
 Matches 104; Conservative 0; Mismatches 21; Indels 0; Gaps 0;

Db 2223 tttttgtgtttttaataagacagaggtttccaccatgtggcaggctggtctcaaacctc 2282  
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

Cp 1715 TTTTTCCTTTTAAATTGAGATGGAGTTTCACCTGTGTGTATGAGGCTGGTCTCAAACTCC 1656

Db 2283 tgacctcaagtaataccactgctcgtcgtcccaaaagtctgggtatcacaggatgagcc 2342  
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

Cp 1655 CGAGCTCAGCAATCCACCTGCTCAGCCTATCAAGTCTGGGATTACAGGCATGAGCC 1596

Db 2343 accgc 2347  
 |||||

Cp 1595 ACCGC 1591

RESULT 6  
 ID Q92781 standard; DNA; 3234 BP.  
 AC Q92781;

DT 09-DEC-1995 (first entry)  
 DE Human thymopoietin gene fragment.  
 KW Thymopoietin; diagnostic; therapeutic; gene therapy; ss.  
 OS Homo sapiens.  
 FH Key Location/Qualifiers  
 FT exon 1..54  
 FT /\*tag= a  
 FT /note= '3' end of exon 6'  
 FT exon 1357..1445  
 FT /\*tag= b  
 FT /note= 'exon 7'  
 FT exon 2572..3234  
 FT /\*tag= c  
 FT /note= 'exon 8 - partial sequence'  
 PN M05517205-A1.  
 PD 29-JUN-1995.  
 PF 13-DEC-1994; U14356.  
 PR 21-DEC-1993; US-171382.  
 PA (HMOU-) IMMUNOBIOLOGY RES INST INC.  
 PI Culler MD, Goldstein G, Harris CA, Setcavage DR;  
 PI Shenbagamurthi P, Slekierka JJ, Talle NA;  
 DR WPI; 95-240474/31.  
 PT Polynucleotide(s) encoding human thymopoietin proteins - used to  
 PT develop prods. for diagnosis and therapy involving immune or nervous  
 PT system conditions.  
 PS Disclosure; Fig 11a-11c; 85pp; English.  
 CC The sequence represents a fragment of the human thymopoietin gene,  
 CC including the 3' end of exon 6, exon 7 and a partial sequence for  
 CC exon 8. DNA encoding human thymopoietin, isolated from  
 CC a cDNA library prepared from human thymus RNA, may be expressed in  
 CC a host cell e.g. bacterium (preferably Escherichia coli), fungus,  
 CC insect or mammalian cell for production of recombinant thymopoietin.  
 CC Thymopoietin has a regulatory effect on the mammalian immune system,  
 CC and can be used for treating/modulating an immune or nervous system  
 CC condition, and for the treatment of chronic infection, autoimmune  
 CC disorders and certain affective psychiatric or neurological  
 CC disorders. The protein and the DNA can be used as diagnostics;  
 CC the DNA can be used in gene therapy.  
 SQ Sequence 3234 BP; 933 A; 577 C; 617 G; 1107 T;

Query Match 4.0%; Score 84; DB 15; Length 3234;  
 Best Local Similarity 80.94; Pred. No. 2.07e-38;  
 Matches 110; Conservative 0; Mismatches 26; Indels 0; Gaps 0;

Db 898 tttttgtatttttagatagagtggttccactgtgtgtcaggctggtctgaacctc 957  
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

Cp 1715 TTTTTCCTTTTAAATTGAGATGGAGTTTCACCTGTGTGTATGAGGCTGGTCTCAAACTCC 1656

Db 958 tgacctcaggtatgccaccgctcagcctcccaaaagtctgggtatcacaggatgagcc 1017  
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

Cp 1655 CGAGCTCAGCAATCCACCTGCTCAGCCTATCAAGTCTGGGATTACAGGCATGAGCC 1596

Db 1018 accgtaccggcccaaa 1033  
 ||||| ||||| |||||

Cp 1595 ACCGCATGTGGCTTAA 1580

RESULT 7  
 ID Q10572 standard; DNA; 1047 BP.  
 AC Q10572;  
 DT 09-APR-1991 (first entry)  
 DE Human Natriuretic Peptide Receptor B.  
 KW NPRB; ANP; BNP; CNP; kidney failure; heart failure; protein kinase;  
 KW hyperaldosteronism; glaucoma; guanyl cyclase.  
 OS Homo sapiens.  
 FH Key Location/Qualifiers  
 FT Peptide 1..22  
 FT /label= signal sequence  
 FT Protein 13  
 FT /label= mature NPRB  
 FT Domain 23..455  
 FT /label= extracellular domain  
 FT /note= 'binds natriuretic peptides A,B and C'

Dh	29	vvnvnnhmsyavavrnvgnavanvngnranvndvrvnsnnngscgynnnasvdfv	88
Qy	161	GACTTTGGGGACCAAGCTCTCCGACGCCCTCGAGCGCTCGAGCAGCGGCTATCCAGAG	220
Dh	89	nyhdndnnngscgynnaasvraneshvrnnnttagavagsnsakndhytrtvrtvgsan	148
Qy	221	CCAGGACAGCGTCGGGAACACAGCATGGCTCTCGTGAACCCACAGATCTTAACTTCGTG	280
Dh	149	ngnvnvtr--bghnvnrtaraanvndatddrhnyhtngvnnvnnngssnsvnnhvayr	206
Qy	281	TCCTCATCGTCGGGGTCTCTGTCGGCGTCGGGGTGAATCTGCACCATCCCCGGCAG	340
Dh	207	aggnnathnnaagrayvnc--gnnnnhnnnnnnaarntngdyvnyndvngnsnrag	265
Qy	341	ACGAAGATTCCTCCACAGCAGTGGCCCCACCAACAGAGCGCACGCTCAAGGAGGAG	400
Dh	266	n--ttrgsvndvndtrnnanraan--ann--tvnvtvtrnnnnnnnnnnnnnnrardng	322
Qy	401	AGTGTCCAGCAGGATCTCATAGTCAAGATTAATCTGGAGCGCTGTAACCGCTGCACAGAG	460
Dh	323	vnnngsnmnnnagcnydgynny--avnnvntnngsgtrdgrnrvnkmgrryhtvgvgr	381
Qy	461	GTGTGGATACACATGTCTCCACAAAT7TGCCCTTGCTGCTGTATGTACAGTTGTGA	520
Dh	382	mdknrdnrtvnnvwngdngsdgnnaahysganknvwtygrvnnvkvngansnnncan	441

Qy 521 AATCAGGTCAACAAATAAAGTCTCTGTACACGAGCA - GAGACACCGCTGTGCACTGT 579

Db 442 dnddsdsktstnsvangvgtgtntnnmyssvsnnrknmnknasnmwrvnnnnn 501

Qy 580 GAAAAA - GGAGAGTCTCCAGGATAAAATCCCTCGAGATGTCCGGACCTGTAGAACAGG 638

Db 502 gsnryrhkgsgrtrnsrtnsgysgsmtahkyknnantghnkvrvvankhmknnrnt 561

Qy 639 GTGTCCCGAGGGGTGCTCAAGTCAGTAATTGTACGCCCGGAGTGACATCAAGTCCAA 698

Db 562 rrvnnnknkhrdvnnnhtrngacdnncnvtayvrgnsngndnnndsnndwmyr 621

Qy 699 AAATGAATCACTGCCGTCCACTGTGGAAACCCACGACGAGGAGACAGTGACCAC 758

Db 622 snnn - drvkvmanhnnssnssghsknsncvdsrvnkvtndyngasnrstannndnan 680

Qy 759 CATCTCGGGAGTCTTGCTCTCCCTACTACTACTATATCAATCATGTGTTTGGTACT 818

Db 681 yakknntannnsnnntnngmaadvysngnnnnnnnsgnyngndnsnkvnkv 740

Qy 819 CATTTAGCTGTGTTGTGTTGCTTTTCATCTGGAGAAATCATTTCTACTCA 878

Db 741 rgnrnyrnnsndrtnnnnnnvnmrnwcdanrnnngnkngrnnrknagtsnda 800

Qy 879 AGGCATCTGCTCAGGTGTGGAGAGAGTCCGAGCTGTGCACAGATCTCTT - TCCGCG 937

Db 801 nnrnmyannnnkvnnrntaynnrknknanaynnnnhsvannknrgtvnandsv 860

Qy 938 GGGGCTCATGTCCTTCCAGAGTCTCGGGCGAGGACAACTGGCCGAACGAGACCTGA 997

Db 861 taynsndvngtansnsntnmrvtnndndytcndannndndykvntngdmyvsvng 920

Qy 989 GTACACAGATACTTCGACGCCACC - CAGGTGCTTGAGCAGAGAACTCAAGGTCAGAGCTC 1056

Db 921 rgnrphannnarnnandavssnrhrhndnrrnngvhtngvcagvgymkrryno 980

Qy 1057 GCAGAGCTAACAGGTGTGATCTAGAGTGTCCGAGAGGACCCAGCGCTCTCTGGAAC 1116

Db 981 gdtvtnsrmnsgnankhvsvtkdandngc 1014

Qy 1117 GCAGAGCTGAGGGGTGTCAGAGAGGAGGCTGC 1150

```

RESULT      8
ID   Q10572 standard; DNA; 1047 BP.
AC   Q10572;
DC   09-APR-1991 (first entry)
DE   Human Natriuretic Peptide Receptor B.
KW   NPBR; ANP; BNP; CNP; kidney failure; heart failure; protein kinase;
KW   hyperaldosteronism; glaucoma; guanyl cyclase.
OS   Homo sapiens.
PH   Key                               Location/Qualifiers
FT   Peptide                           1..22
FT   /label= signal sequence
FT   Protein                           12
FT   /label= mature NPBR
FT   Domain                            23..455
FT   /label= extracellular domain
FT   /note= "binds natriuretic peptides A,B and C]"
FT   Domain                            456..456
FT   /label= transmembrane domain
FT   Domain                            479..1047
FT   /label= cytoplasmic domain
FT   /note= "GC and protein kinase activity"
FT   Modified-site 24..26
FT   /label= N-glycos_site
FT   Modified-site 35..37
FT   /label= N-glycos_site
FT   Modified-site 161..163
FT   /label= N-glycos_site
FT   Modified-site 195..197
FT   /label= N-glycos_site
FT   Modified-site 244..246

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Query Match 3.9%; Score 81; DB 7; Length 1618;  
Best Local Similarity 79.1%; Pred. No. 2.42e-36;

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Query Match          3.9%; Score 82; DB 7; Length 17327;
Best Local Similarity 83.1%; Pred. No. 4.96e-37;
Matches 103; Conservative; 0; Mismatches 21; Indels 0; Gaps 0;

Db 11013 gccacgtgtgtggcttcgcctgtaatccgaacatttggaggccgagcgaggagat 11072
Qv 1584 gccacatccggctggctcatcgctgtatcccgacac77tgaaggctgagcgaggat 1643

```



Db	89	ggtggctcatcctgctaaacccagacatctgggaagctgagcgaggaattgctgaac	148
Qy	1593	GGTGGCTCATCGCTGTAATCCAGCACTTATGATAGGCTGAGGACAGGTGATGCTTGAG	1652
Db	149	ccagagatttgacatcagctggcgcaactggtgaaccccactctcaaaaaattgcaa	208
Qy	1653	TCGGGATTGTGACACGCGCTCATCAACACAGTGAAATCCATCTCAATTTAAAAAGAA	1712
Db	209	aaa	211
Qv	1713	AAA	1715

RESULT 14  
ID Q75209 standard; cDNA; 8342 BP.

AC Q75209;  
DT 23-AUG-1995 (first entry)  
DE ALL-1 (acute lymphocytic leukaemia-1) breakpoint cluster region.  
KW Acute lymphoblastic leukaemia; acute nonlymphoblastic leukaemia;  
KW chromosomal translocation; abnormality; detection; rearrangement;  
KW breakpoint cluster region; Alu repeat; chromosome 11; probe B859; ds.  
OS Homo sapiens.

FH Key Location/Qualifiers  
FT exon 1..263

FT /\*tag= a  
FT /number= 5  
FT intron 264..2352  
FT /\*tag= b  
FT exon 593..666

FT /\*tag= c  
FT /number= 6  
FT intron 667..798  
FT /\*tag= d  
FT repeat\_unit 799..1108

FT /\*tag= e  
FT /rpt\_type= OTHER  
FT /note= "Alu repeat-a (Class J)"  
FT repeat\_unit 1119..1420

FT /\*tag= f  
FT /rpt\_type= OTHER  
FT /note= "Alu repeat-b (Class Sx)"  
FT repeat\_unit 1432..1716

FT /\*tag= g  
FT /rpt\_type= OTHER  
FT /note= "Alu repeat-c (Class Sb0)"  
FT repeat\_unit 1921..2216

FT /\*tag= h  
FT /rpt\_type= OTHER  
FT /note= "Alu repeat-d (Class J)"  
FT exon 2353..2484

FT /\*tag= i  
FT /number= 7  
FT intron 2485..3031  
FT /\*tag= j  
FT exon 3032..3145

FT /\*tag= k  
FT /number= 8  
FT intron 3146..6787  
FT /\*tag= l  
FT repeat\_unit 3973..4268

FT /\*tag= m  
FT /rpt\_type= OTHER  
FT /note= "Alu repeat-e (Class Sb0)"  
FT repeat\_unit 4764..5094

FT /\*tag= n  
FT /rpt\_type= OTHER  
FT /note= "Alu repeat-f (Class J)"  
FT repeat\_unit 6072..6362

FT /\*tag= o  
FT /rpt\_type= OTHER  
FT /note= "Alu repeat-g (Class S)"  
FT exon 6788..6934

FT /\*tag= p  
FT /number= 9  
FT intron 6935..7966  
FT /note= "nucleotides 7429-7559 show about 80%  
sequence identity to genomic sequences  
found in 5' regulatory regions, 3' segments,  
or in introns of several genes such as ApoA4,  
Factor VIIIc subunit and G6PD"

FT /\*tag= q  
FT repeat\_unit 7164..7427  
FT /\*tag= r  
FT /rpt\_type= OTHER  
FT /note= "Alu repeat-h (Class Sx)"  
FT exon 7967..8062

FT /\*tag= s  
FT /number= 10  
FT intron 8063..8303  
FT /\*tag= t  
FT exon 8304..8342  
FT /\*tag= u  
FT /number= 11  
PN W09426930-A.  
PD 24-NOV-1994.  
PF 22-APR-1994; U04496.  
PR 14-MAY-1993; US-062443.  
PA (UTJE-) UNIV JEFFERSON THOMAS.  
PI Canaan E, Croce C;  
DR WPI: 95-006818/01.  
DR P-PSDB: R66467.

FT New acute lymphocytic leukaemia gene prods. - used for the  
FT diagnosis and treatment of leukaemias, partic. acute  
FT lymphoblastic or nonlymphoblastic leukaemia  
PS Example 5; Fig 22; 207pp; English.  
CC A phage clone, mgl1.1, which spans the breakpoint cluster region in  
CC the ALL-1 gene has been sequenced (Q75209). Eight Alu repeat  
CC sequences were identified and classified based on criteria  
CC published in Milosavljevic et al. (J.Mol.Evol. 32, 105-121, 1991).  
CC The high concentration of Alu sequences within the area spanned by  
CC exons 6 and 7 suggested a possible role for Alu in the chromosomal  
CC translocations involving the ALL-1 gene. Homologous recombination  
CC is not involved so the Alu repeats may act indirectly by  
CC destabilising the region.  
SQ Sequence 8342 BP; 2604 A; 1613 C; 1758 G; 2367 T;

Query Match 3.8%; Score 79; DB 13; Length 8342;  
Best Local Similarity 81.1%; Pred. No. 5.73e-35;  
Matches 103; Conservative 0; Mismatches 24; Indels 0; Gaps 0;

Db 4771 tgcacgttgctcagcgtctgaatccacgtactcttgaggagcagcagagaccgcttg 4830

Qy 1590 TCGCGTGCTCTGCTCTGTAATCCACGACCTTTGATAGGCTGAGGCGTGATGCTTG 1649

Db 4831 agctcaggaggttcacagacagcgtcagacacacatagtcagcctcattctactaaaaaa 4890

Qy 1650 AGCTCGGAGGTTTGAGACCGAGCTCATACACAGCTGAACCTCCATCTCAATTTAAAAG 1709

Db 4891 aaataaa 4897

Qy 1710 AAAAAA 1716

RESULT 15  
ID T16333 standard; DNA; 8391 BP.

AC T16333;  
DT 29-JUL-1997 (revised)  
DT 06-JUN-1996 (first entry)  
DE MLL gene 8.3 kb fragment encoding all common translocation breakpoints.  
KW MLL; myeloid; lymphoid; leukaemia; probe; chromosome; translocation;  
KW mutation; 11q23; lymphoma; monitoring; ss.  
OS Homo sapiens.

PN US5487970-A.  
PD 30-JAN-1996.  
PF 17-JUN-1992; 900689.  
PR 17-JUN-1992; US-900689.  
PR 16-DEC-1992; US-991244.  
PR 17-JUN-1993; US-080255.  
PA (ARCH-) ARCH DEV CORP.  
PI Diaz MO, Rowley JD;  
DR WPI: 96-105221/11.

PT Detection of 11q23 chromosome translocation(s) - using myeloid/lymphoid  
PT leukaemia nucleic acid probes, for diagnosis and monitoring of  
PT leukaemia(s) and lymphoma(s)  
PS Example 3; Column 49-56; 47pp; English.  
CC T16333 is an 8.3 kb human genomic DNA BamHI fragment of the human MLL  
CC (myeloid/lymphoid leukaemia) gene. This sequence contains all of the  
CC common MLL translocation breakpoints and may be used to map the  
CC intron-exon boundaries within this region and to identify the

WashU-Merck EST Project  
 Estimation School of Medicine  
 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108  
 Tel: 314 286 1800  
 Fax: 314 286 1810  
 Email: est@wustl.edu 249  
 Source: IMAGE Consortium, LLNL  
 This clone is available royalty-free through LLNL; contact the  
 IMAGE Consortium (info@image.llnl.gov) for further information.

FEATURES  
 source  
 location/Qualifiers  
 /organism="Homo sapiens"  
 /clone="150393"  
 BASE COUNT 90 a 104 c 97 g 111 t 5 others  
 ORIGIN  
 Query Match 4.2%; Score 87; DB 12; Length 407;  
 Best Local Similarity 83.2%; Pred. No. 6.15e-107;  
 Matches 109; Conservative 0; Mismatches 22; Indels 0; Gaps 0;  
 Db 135 TTTTGTATTTTGTAGATGAGTGAGTTTCACACATCTTGGCCAGGCTGCTCGAATCC 194  
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||  
 Cp 1715 TTTTTCCTTTTAAATTGAGTGAGTTTCATCTGTGTATGATGAGCTGCTCAAACTCC 1656  
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||  
 Db 195 TGACCTCAAGTGTCTGCTGCTGACGCTCCCAAGCTGCTGCGATTAAGCTGTGAGCC 254  
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||  
 Cp 1655 CGAGCTCAAGCAATCACCAGCTGCTGAGCTATCAAGTCTGGGATTAGAGCATGAGCC 1596  
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||  
 Db 255 ACCGACCTGG 265  
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||  
 Cp 1595 ACCGATGGG 1585  
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

Search completed: Fri May 15 18:55:40 1998  
 Job time : 1929 secs.